

```

;
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ. ID NO.: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
;
; US-08-205-697A-22
;
Query Match
Best Local Similarity 30.6%; Score 110; DB 4; Length 1120;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
;
QY 1 ATCAAGGTTACCCAGACCTTAAGAGATGATTTTCAGCTAAACACTGAGAATTCACACT 60
DB 584 ATACAGGGTTACCCAGACCTTAAGAGATGATGTTTCTTAAGAACCAAGATTCACACT 643
QY 61 ACTAAGTATGATTCGTCTCATGTAAGAAATCTCAAAATATATGACAGCACTGTACACGTT 120
DB 644 ATCGATATGATGATGATTTATGCAGAATCTCAAGATTAATGTACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTGTGCC 177
DB 704 TCCATCAGCTTGCTTTTTCATTTCCCTGATGTACAGCAATATGACCATCTTCTGTATT 763
QY 178 CTGAACCTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATAGA 227
DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810
;
RESULT 15
US-08-702-525-22
; Sequence 22, Application US/08702525
; Patent No. 6294660
;
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Bortello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Dee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
;
;

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;
; COUNTRY: USA
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ. ID NO.: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
;
; US-08-702-525-22
;
Query Match
Best Local Similarity 30.6%; Score 110; DB 4; Length 1120;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
;
QY 1 ATCAAGGTTACCCAGACCTTAAGAGATGATTTTCAGCTAAACACTGAGAATTCACACT 60
DB 584 ATACAGGGTTACCCAGACCTTAAGAGATGATGTTTCTTAAGAACCAAGATTCACACT 643
QY 61 ACTAAGTATGATTCGTCTCATGTAAGAAATCTCAAAATATATGACAGCACTGTACACGTT 120
DB 644 ATCGATATGATGATGATTTATGCAGAATCTCAAGATTAATGTACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTGTGCC 177
DB 704 TCCATCAGCTTGCTTTTTCATTTCCCTGATGTACAGCAATATGACCATCTTCTGTATT 763
QY 178 CTGAACCTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATAGA 227
DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810
;
Search completed: October 19, 2002, 23:36:15
Job time : 17.4497 secs

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;
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-479-744A-1

Query Match 30.6%; Score 110; DB 3; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAAGGTTCACGAGACTAGAGATGATTTTCAGCTAAACAGTGAATTCACACT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 ATACAGGTTTACCCAGACCTTAAGAGATGAGTGTTCGTAAGAACCAAGATTCACACT 643
QY 61 ACTAAGTATGATGTCATGATGAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT 120
    | ||||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
DB 644 ATCGAGTATGATGATATTAATCAGAAATCTCAAGATTAATGTACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCGTAG--CACACATGTGAGCGCTTTGTGCC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 704 TCCATCAGCTTGCTGTTTATTCCTGATGATTTACGAGCAATATGACCATCTTCTGTAAT 763
QY 178 CTGAAGTGGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGA 227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 764 CTGAAACTGACA--AGACGGCGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 13
US-08-280-757B-1
; Sequence 1, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CT144/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
```

```
;
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-280-757B-1

Query Match 30.6%; Score 110; DB 3; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAAGGTTCACGAGACTAGAGATGATTTTCAGCTAAACAGTGAATTCACACT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 ATACAGGTTTACCCAGACCTTAAGAGATGAGTGTTCGTAAGAACCAAGATTCACACT 643
QY 61 ACTAAGTATGATGTCATGATGAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT 120
    | ||||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
DB 644 ATCGAGTATGATGATATTAATCAGAAATCTCAAGATTAATGTACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCGTAG--CACACATGTGAGCGCTTTGTGCC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 704 TCCATCAGCTTGCTGTTTATTCCTGATGATTTACGAGCAATATGACCATCTTCTGTAAT 763
QY 178 CTGAAGTGGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGA 227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 764 CTGAAACTGACA--AGACGGCGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 14
US-08-205-697A-22
; Sequence 22, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
```

```

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-456-104-1

Query Match      30.6%; Score 110; DB 2; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTATCCCAAGACCTAAGAGATGTTTTCAGCTAAACCTGAGATTCACT 60
DB 584 ATACAGGTATCCCAAGACCTAAGAGATGTTTTCAGCTAAACCTGAGATTCACT 643
QY 61 ACTAGATGATGATGTCATGATGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 120
DB 644 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
DB 704 TCCATCAGCTTGTCTGTTTCATTCCTGATGTTACGAGCAATATGACCATCTCTGATAT 763
QY 178 CTGAAGCTGAGACACTGAGATGCGCTGCTCCCTACCTTTCAATATAGA 227
DB 764 CTGGAAGCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 11
US-08-101-624-1
; Sequence 1, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
```

```

; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-101-624-1

Query Match      30.6%; Score 110; DB 2; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTATCCCAAGACCTAAGAGATGTTTTCAGCTAAACCTGAGATTCACT 60
DB 584 ATACAGGTATCCCAAGACCTAAGAGATGTTTTCAGCTAAACCTGAGATTCACT 643
QY 61 ACTAGATGATGATGTCATGATGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 120
DB 644 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
DB 704 TCCATCAGCTTGTCTGTTTCATTCCTGATGTTACGAGCAATATGACCATCTCTGATAT 763
QY 178 CTGAAGCTGAGACACTGAGATGCGCTGCTCCCTACCTTTCAATATAGA 227
DB 764 CTGGAAGCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 12
US-08-479-744-1
; Sequence 1, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; City: Boston
; STATE: Massachusetts
```

```

US-09-039-641-33
: Sequence 33, Application US/09039641
: Patent No. 6251627
: GENERAL INFORMATION:
: APPLICANT: Cal, Zeling
: APPLICANT: Sprent, Jonathan
: APPLICANT: Brumark, Anders
: APPLICANT: Jackson, Michael
: APPLICANT: Peterson, Per A.
: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
: TITLE OF INVENTION: ACTIVATION OF T-CELLS
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Olson & Hierrl, Ltd.
: STREET: 20 No. 6251627th Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/039,641
: FILING DATE: 8-MAR-1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Olson, Arne M.
: REGISTRATION NUMBER: 30,203
: REFERENCE/DOCKET NUMBER: TSRI4710
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 580-1180
: TELEFAX: (312) 580-1189
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1002 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: US-09-039-641-33

Query Match          30.6%; Score 110; DB 4; Length 1002;
Best Local Similarity 73.5%; Pred. No. 2.5e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACCTTAAGAGATGTTTTCAGCTTAACACTGAGATTCAACT 60
DB 484 ATACAGGTTACCCAGAACCTTAAGAGATGTTTTCAGCTTAAGAACCAAGATTCAACT 543
QY 61 ACTAAGTATGATGCTGTCATGAAGAATCTCAAAATTAATGTCAGACAACTGTACAGCTT 120
DB 544 ATCGAGTATGATGTTATGTCAGAAATCTCAAGATTAATGTCAGACAACTGTACAGCTT 603
QY 121 TCTATCAGTTCGCTTTTTCAGTCCCTGAG---CACACAATGAGCGCTCTTTGTGCC 177
DB 604 TCCATCAGTTCGCTTTTTCAGTCCCTGAGTTCAGACCAATATACCATCTTCTGTATT 663
QY 178 CTGAACCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
DB 664 CTGGAACCTGACA---AGACGGCGCTTTTATCTTACACCTTTCTATATAGA 710

RESULT 9
US-09-039-762A-33
: Sequence 33, Application US/09039762A
: Patent No. 6255073
: GENERAL INFORMATION:
: APPLICANT: Cal, Zeling

```

```

: APPLICANT: Sprent, Jonathan
: APPLICANT: Brumark, Anders
: APPLICANT: Jackson, Michael
: APPLICANT: Peterson, Per A.
: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
: TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Olson & Hierrl, Ltd.
: STREET: 20 No. 6255073th Wacker Drive, 36th Floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/039,762A
: FILING DATE: 16-MAR-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OLSON, Arne M.
: REGISTRATION NUMBER: 30,203
: REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 580-1180
: TELEFAX: (312) 580-1189
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1002 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: US-09-039-762A-33

Query Match          30.6%; Score 110; DB 4; Length 1002;
Best Local Similarity 73.5%; Pred. No. 2.5e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACCTTAAGAGATGTTTTCAGCTTAACACTGAGATTCAACT 60
DB 484 ATACAGGTTACCCAGAACCTTAAGAGATGTTTTCAGCTTAAGAACCAAGATTCAACT 543
QY 61 ACTAAGTATGATGCTGTCATGAAGAATCTCAAAATTAATGTCAGACAACTGTACAGCTT 120
DB 544 ATCGAGTATGATGTTATGTCAGAAATCTCAAGATTAATGTCAGACAACTGTACAGCTT 603
QY 121 TCTATCAGTTCGCTTTTTCAGTCCCTGAG---CACACAATGAGCGCTCTTTGTGCC 177
DB 604 TCCATCAGTTCGCTTTTTCAGTCCCTGAGTTCAGACCAATATACCATCTTCTGTATT 663
QY 178 CTGAACCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
DB 664 CTGGAACCTGACA---AGACGGCGCTTTTATCTTACACCTTTCTATATAGA 710

RESULT 10
US-08-456-104-1
: Sequence 1, Application US/08456104
: Patent No. 5861310
: GENERAL INFORMATION:
: APPLICANT: Freeman, Gordon J.
: APPLICANT: Nadler, Lee M.
: APPLICANT: Gray, Gary S.
: TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:

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Db 544 ATGAGATATGATGATATGAGAAATCTCAGATATATGTCACAGACTGATGACGCTT 603
 QY 121 TCTATCAGCTTGCCTTTTATAGTCCCTGAG--CACAAGTGTAGGCTCTTTGTGCG 177
 Db 604 TCCATCAGCTTGTCTGTTTCATTCCCTGATTTACGAGAAATGACCATCTCTGTATT 663
 QY 178 CTGAAGCTGAGACATGCTGCTCCCTACCTTCAATATAGA 227
 Db 664 CTGAAGCTGACA--AGACGGCGCTTTATCTTACACTTCTCTATAGA 710

RESULT 6
 US-08-848-760B-11
 ; Sequence 11, Application US/08848760B
 ; Patent No. 6248721

GENERAL INFORMATION:

APPLICANT: Chang, Lung-Ji
 TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: United States of America

ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/848,760B
 FILING DATE: 25-Jan-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/838,702

FILING DATE: 09-APR-1997

ATTORNEY/AGENT INFORMATION:
 NAME: PACE, DORAN R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: CNG-100C1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 972 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-08-848-760B-11

Query Match 30.6%; Score 110; DB 4; Length 972;
 Best Local Similarity 73.5%; Pred. No. 2.5e-25;

Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACTAAGAGATGATTTTACGTAACACTGGAATTCACACT 60
 Db 460 ATACAGGTTACCCAGAACTAAGAGATGATTTTTCGTAAGAACCAAGAAATTCACACT 519
 QY 61 ACTAAGTATGATCTGATGATGAGAAATCTCAAAATATGTGACAGACTGTCAACGTT 120
 Db 520 ATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
 QY 121 TCTATCAGCTTGCCTTTTATAGTCCCTGAG--CACAAGTGTAGGCTCTTTGTGCG 177
 Db 580 TCSATCAGCTTGTCTGTTTCATTCCCTGATGTATGACGACAAATATGACACTCTTGTATT 639

QY 178 CTGAAGCTGAGACACTGAGATGCTCTCTCCCTACCTTTCAATATAGA 227
 Db 640 CTGAAGCTGACA--AGACGGCGCTTTATCTTACACTTCTCTATAGA 686

RESULT 7
 US-09-039-982A-33
 ; Sequence 33, Application US/09039982A
 ; Patent No. 6225042

GENERAL INFORMATION:

APPLICANT: Cal, Zelling

APPLICANT: Sprent, Jonathan

APPLICANT: Brummark, Anders

APPLICANT: Jackson, Michael

APPLICANT: Peterson, Per A

TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Olson & Hieryl, Ltd.

STREET: 20 No. 6225042th Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/039,982A

FILING DATE: 16-MAR-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Olson, Arne M.

REGISTRATION NUMBER: 30,203

REFERENCE/DOCKET NUMBER: TSRI4710

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 580-1180

TELEFAX: (312) 580-1189

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 1002 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-039-982A-33

Query Match 30.6%; Score 110; DB 4; Length 1002;
 Best Local Similarity 73.5%; Pred. No. 2.5e-25;
 Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACTAAGAGATGATTTTACGTAACACTGGAATTCACACT 60
 Db 460 ATACAGGTTACCCAGAACTAAGAGATGATTTTTCGTAAGAACCAAGAAATTCACACT 543
 QY 61 ACTAAGTATGATCTGATGATGAGAAATCTCAAAATATGTGACAGACTGTCAACGTT 120
 Db 544 ATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
 QY 121 TCTATCAGCTTGCCTTTTATAGTCCCTGAG--CACAAGTGTAGGCTCTTTGTGCG 177
 Db 604 TCCATCAGCTTGTCTGTTTCATTCCCTGATGTATGACGACAAATATGACACTCTTGTATT 663
 QY 178 CTGAAGCTGAGACACTGAGATGCTCTCTCCCTACCTTTCAATATAGA 227
 Db 664 CTGAAGCTGACA--AGACGGCGCTTTATCTTACACTTCTCTATAGA 710

RESULT 8

QY 1 ATTCAGGCTTACCCGAACCTTAAGGAGATGTATTTCACCTAACACATCGAATTCACACT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 484 ATTCAGGCTTACCCGAACCTTAAGGAGATGTATTTCACCTAACACATCGAATTCACACT 543
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 ACTAAAGTATGATACCTGTATATAGAAGTCTCAATAATATGTGCAGCAACTGTACACGTT 120
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Db 544 ATGCAGTATGATGGTATATATGCAGAAATCTCAGATTAATGTACAGAACTGTACAGGTT 603
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OY 121 TCTATAGCTTGCCCTTTTTCAGTCCCCTGAAG---CACACAATGTAGAGCTCTTTTGGCC 177
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Db 604 TCCATATAGCTTGCTGTTTCATCTCCGTGATGTAAAGCAATATGACCATCTCTCTGATTT 665
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OY 178 CTGAACCTGGAGACACACTGGAATCTCTCTCTCCCATCTTCAATATAGA 227
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Db 664 CTGGAACCTGACA---AGACCGGCGCTTTTATCTTCACACTTTGCTATAGA 710

RESULT 5
US-09-039-762A-34
Sequence 34, Application US/09039762A
Patent No. 6255073

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1  RESULT 5
2  US-09-039-762A-34
3  : Sequence 34, Application US/09039762A
4  : Patent No. 6255073
5  :
6  : GENERAL INFORMATION:
7  : APPLICANT: Cai, Zeling
8  : APPLICANT: Sprent, Jonathan
9  : APPLICANT: Brumark, Anders
10 : APPLICANT: Jackson, Michael
11 : APPLICANT: Peterson, Per A.
12 : TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
13 : FOR ACTIVATION OF T-CELLS
14 :
15 : NUMBER OF SEQUENCES: 59
16 : CORRESPONDENCE ADDRESS:
17 : ADDRESSEE: Olson & Hjerl, Ltd.
18 : STREET: 20 No. 6255073th Wacker Drive, 36th Floor
19 : CITY: Chicago
20 : STATE: Illinois
21 : COUNTRY: USA
22 :
23 : ZIP: 60606
24 :
25 : COMPUTER READABLE FORM:
26 : MEDIUM TYPE: Floppy disk
27 : COMPUTER: IBM PC compatible
28 : OPERATING SYSTEM: PC-DOS/MS-DOS
29 : SOFTWARE: PatentIn Release #1.0, Version #1.25
30 :
31 : CURRENT APPLICATION DATA:
32 : APPLICATION NUMBER: US/09/039,762A
33 : FILING DATE: 16-MAR-1998
34 : CLASSIFICATION: 435
35 : ATTORNEY/AGENT INFORMATION:
36 : NAME: OLSON, Arne M.
37 : REGISTRATION NUMBER: 30,203
38 : REFERENCE/DOCKET NUMBER: TSHI 471.0 DIV.2
39 :
40 : TELECOMMUNICATION INFORMATION:
41 : TELEPHONE: (312) 580-1180
42 : TELEFAX: (312) 580-1189
43 : INFORMATION FOR SEQ ID NO: 34:
44 : SEQUENCE CHARACTERISTICS:
45 : LENGTH: 751 base pairs
46 : TYPE: nucleic acid
47 : STRANDEDNESS: double
48 : TOPOLOGY: linear
49 : MOLECULE TYPE: cDNA
50 : HYPOTHETICAL: NO
51 : ANTI-SENSE: NO
52 :
53 : US-09-039-762A-34
54 :
55 : Query Match 30.6%; Score 110; DB 4; Length 751;
56 : Best Local Similarity 73.5%; Pred. No. 2, 2e-25;
57 : Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2
58 :
59 : 1 ATACAGGTTATCCACAGACCTAAGAGATGTATTTTCAGCTAAACCTGAGATTCAACT 60
60 : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 : Db 484 ATACAGGTTATCCACAGACCTAAGAGATGTATTTTCAGCTAAGAACCAAGATTCAACT 543
62 :
63 : 51 ATACAGGTTATCCACAGACCTAAGAGATGTATTTTCAGCTAAGAACCAAGATTCAAGGTT 120

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4C-W706-650-03-03-34

4C-W706-650-03-03-34

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 12.4497 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggttaccagacc.....ggcgacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	30.6	306	3 US-08-479-744A-46	Sequence 46, Appl
2	110	30.6	306	3 US-08-280-757B-46	Sequence 46, Appl
3	110	30.6	751	4 US-09-039-982A-34	Sequence 34, Appl
4	110	30.6	751	4 US-09-039-641-34	Sequence 34, Appl
5	110	30.6	751	4 US-09-039-762A-34	Sequence 34, Appl
6	110	30.6	972	4 US-08-848-760B-11	Sequence 11, Appl
7	110	30.6	1002	4 US-09-039-982A-33	Sequence 33, Appl
8	110	30.6	1002	4 US-09-039-641-33	Sequence 33, Appl
9	110	30.6	1002	4 US-09-039-762A-33	Sequence 33, Appl
10	110	30.6	1120	2 US-08-456-104-1	Sequence 1, Appl
11	110	30.6	1120	2 US-08-101-624-1	Sequence 1, Appl
12	110	30.6	1120	3 US-08-479-744A-1	Sequence 1, Appl
13	110	30.6	1120	3 US-08-280-757B-1	Sequence 1, Appl
14	110	30.6	1120	4 US-08-205-697A-22	Sequence 22, Appl
15	110	30.6	1120	4 US-08-702-525-22	Sequence 22, Appl
16	110	30.6	1120	4 US-08-403-253A-3	Sequence 3, Appl
17	110	30.6	1120	5 PCT-US95-02576-22	Sequence 22, Appl
18	110	30.6	1161	4 US-08-702-525A-24	Sequence 24, Appl
19	110	30.6	1161	4 US-08-702-525-24	Sequence 24, Appl
20	110	30.6	1161	5 PCT-US95-02576-24	Sequence 24, Appl
21	110	30.6	1424	4 US-09-326-186B-226	Sequence 226, App
22	110	30.6	1428	5 PCT-US94-09642-1	Sequence 1, Appl
23	110	30.6	210	4 US-08-205-697A-31	Sequence 31, Appl
24	78	21.7	210	4 US-08-702-525-31	Sequence 31, Appl
25	78	21.7	210	5 PCT-US95-02576-31	Sequence 31, Appl
26	77.2	21.5	1151	4 US-08-456-104-3	Sequence 3, Appl
27	77.2	21.5	1151	4 US-08-205-697A-20	Sequence 20, Appl

28	77.2	21.5	1151	4 US-08-702-525-20	Sequence 20, Appl
29	77.2	21.5	1151	5 PCT-US95-02576-20	Sequence 20, Appl
30	77.2	21.5	1163	3 US-08-479-744A-22	Sequence 22, Appl
31	77.2	21.5	1163	3 US-08-280-757B-22	Sequence 22, Appl
32	77.2	21.5	1261	4 US-08-205-697A-12	Sequence 12, Appl
33	77.2	21.5	1261	4 US-08-702-525-12	Sequence 12, Appl
34	77.2	21.5	1261	5 PCT-US95-02576-12	Sequence 12, Appl
35	31.2	8.7	740	4 US-09-342-681C-99	Sequence 213, App
36	30	8.4	1978	4 US-08-936-165A-213	Sequence 3, Appl
37	30	8.4	2351	4 US-09-276-531-3	Sequence 24, Appl
38	30	8.4	4865	3 US-08-894-017-24	Sequence 6, Appl
39	29.8	8.3	785	3 US-09-008-979A-6	Sequence 6, Appl
40	29.8	8.3	785	4 US-09-460-618-6	Sequence 1, Appl
41	29.6	8.2	2215	2 US-08-980-329C-1	Sequence 1, Appl
42	29.4	8.2	14683	2 US-08-819-866-1	Sequence 1, Appl
43	29.4	8.2	14683	2 US-09-023-715-1	Sequence 1, Appl
44	29.2	8.1	263	3 US-09-157-177-121	Sequence 121, App
45	29.2	8.1	1371	2 US-08-428-713-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-479-744A-46
Sequence 46, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

PS Claim 1; Page 121-123; 148bp; English.
XX
PS The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;

Query Match 63.3%; Score 227.2; DB 20; Length 2830;
Best Local Similarity 94.8%; Pred. No. 4.1e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACAAGTGAATTCACCT 60
DB 2169 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACAAGTGAATTCACCT 2110
OY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 120
DB 2109 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 2050
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGACGCTTTTGTGCCCTG 180
DB 2049 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGACGCTTTTGTGCCCTG 1990
OY 181 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATCAAAAG 240
DB 1989 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGATGACAACTAAG 1930
OY 241 GAGAGAAA 248
DB 1929 GATPAAGA 1922

RESULT 15
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ID AAZ27915 standard; DNA: 987 BP.
XX
AC AAZ27915;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2 protein coding sequence.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
OS
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
DR P-PSDB; AAY41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
treating, e.g. autoimmune and atopic diseases

XX
PS Claim 1; Page 102-103; 148bp; English.
XX
PS The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 47.2%; Score 169.4; DB 20; Length 987;
Best Local Similarity 87.2%; Pred. No. 3.4e-40;
Matches 198; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

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DB 481 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACAAGTGAATTCACCT 540
OY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 120
DB 541 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 600
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGACGCTTTTGTGCCCTG 180
DB 601 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGACGCTTTTGTGCCCTG 660
OY 181 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATCAAAAG 227
DB 661 CAACCTGAGTCAAT--GAAGCTTCCCTCCCTACCTTATATATAGAA 704

Search completed: October 19, 2002, 23:33:38
Job time : 60.4731 secs

CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
 CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
 CC herpesvirus, feline Borna disease virus, rabies virus, chlamydia,
 CC toxoplasmosis gondii, dirofilaria immitis, or a flea, bacterial
 CC pathogen, or parasite (all claimed). Vaccines capable of
 CC enhancing an immune response, and vaccines capable of suppressing
 CC an immune response (suitable for treating an autoimmune disease
 CC or tissue or organ transplant rejection) are claimed. The
 CC nucleic acids may be used for gene therapy or antisense therapy
 CC protocols.

XX
 SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

Query Match 63.3%; Score 227.2; DB 21; Length 1080;
 Best Local Similarity 94.8%; Pred. No. 2.9e-57;
 Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTTATTTTCAGCTAAACACTGAGAAATTCACCT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 546 ATACAGGTTACCCAGAACCTAAGAGATGTTATTTTCAGCTAAACACTGAGAAATTCACCT 605
 QY 61 ACTAAGTATGATCTGTCATGGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 606 ACTAAGTATGATCTGTCATGGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 665
 QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGGCGCTTTTGTGCCCTG 180
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 Db 666 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGGCGCTTTTGTGCCCTG 725
 QY 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCTCAAAAG 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 726 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCTCAAAAG 785
 QY 241 GAGAGAAA 248
 || || ||
 Db 786 GATTAAGA 793

RESULT 13

AA227929
 ID AA227929 standard; DNA; 2830 BP.

XX AA227929;

XX 20-DEC-1999 (first entry)

XX Feline B7-2 protein encoding DNA.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; feline;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Felis catus.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Slim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX P-PSDB; AAY41079.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

XX treating, e.g. autoimmune and atopic diseases

PS Claim 1; Page 116-119; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.

XX
 SQ Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match 63.38%; Score 227.2; DB 20; Length 2830;
 Best Local Similarity 94.8%; Pred. No. 4.1e-57;
 Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTTATTTTCAGCTAAACACTGAGAAATTCACCT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 662 ATACAGGTTACCCAGAACCTAAGAGATGTTATTTTCAGCTAAACACTGAGAAATTCACCT 721
 QY 61 ACTAAGTATGATCTGTCATGGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 722 ACTAAGTATGATCTGTCATGGAAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTT 781
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 Db 782 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGGCGCTTTTGTGCCCTG 841
 QY 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCTCAAAAG 240
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 Db 842 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCTCAAAAG 901
 QY 241 GAGAGAAA 248
 || || ||
 Db 902 GATTAAGA 909

RESULT 14

AA227930/C
 ID AA227930 standard; DNA; 2830 BP.

XX AA227930;

XX 20-DEC-1999 (first entry)

XX Feline B7-2 gene complementary DNA sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; feline;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Felis catus.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Slim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

XX treating, e.g. autoimmune and atopic diseases

XX	AAZ34838:
AC	
XX	28-FEB-2000 (first entry)
DT	
XX	
DE	Feline CD86 (B7-2) cDNA.
XX	
KM	CD86; B7-2; feline; cat; recombinant virus; vaccine;
KM	immunomodulator; tumour; cancer; therapy; ss.
XX	
OS	Felis domesticus.
XX	
FT	Key Location/Qualifiers
FT	CDS 63..1052
FT	/**tag= a
XX	
PN	W09957295-A1.
XX	
PD	11-NOV-1999.
XX	
PF	30-APR-1999; 99WO-US050504.
XX	
PR	01-MAY-1998; 98US-0071711.
XX	
PA	(SCHE) SCHERING-PLOUGH LTD.
PA	(SCHE) SCHERING-PLOUGH VETERINARY CORP.
XX	
PI	Winslow BJ, Cochran MD;
XX	
DR	WPI: 2000-062155/05.
DR	P-PSDB; AAY32285.
XX	
PT	Novel recombinant virus useful as immunomodulators, particularly in
PT	vaccines -
XX	
PS	Disclosure; Fig 3A; 230pp; English.
XX	
CC	This is the nucleotide sequence of cDNA coding for feline CD86
CC	(B7-2). The cDNA was isolated from feline peripheral blood
CC	mononuclear cell cDNA by PCR. Manipulating the expression of CD28
CC	or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC	regulates T cell proliferation and cytokine release. The invention
CC	relates to a recombinant virus that contains at least one foreign
CC	nucleic acid, inserted into a nonessential genomic region, that
CC	encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
CC	immunogenic fragments, and is expressed when the recombinant virus
CC	is introduced into a suitable host. The invention also provides:
CC	a recombinant virus further comprising a foreign nucleic acid
CC	encoding an immunogen derived from a feline pathogen; recombinant
CC	viruses capable of enhancing an immune response to protect against
CC	disease; recombinant viruses expressing antisense sequences,
CC	capable of suppressing an immune response in a feline, e.g. for
CC	treatment of autoimmune disease or transplant rejection; and
CC	recombinant viruses expressing DNA encoding CD80 and/or CD86 used
CC	to reduce or eliminate a tumour in cats.
XX	
SQ	Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
	Query Match 63.3%; Score 227.2; DB 21; Length 1080;
	Best Local Similarity 94.8%; Pred. No. 2,9e-57;
	Matches 235; Conservative % 0; Mismatches 13; Indels 0; Gaps
QY	1 ATACAGGTTTCCCAAGAACCTTAAGAGATGTATTTCAGCTAAACAOTGAGATTGAAC 60
DB	
546	ATACAGGTTTCCCAAGAACCTTAAGAGATGTATTTCAGCTAAACAOTGAGATTGAAC 605
QY	61 ACTAGTGATGATAGTATGATAGAATAATCTCAAAATATGTGACAGAACTGTCACAGTT 120
DB	
606	ACTAGTGATGATAGTATGATAGAATAATCTCAAAATATGTGACAGAACTGTCACAGTT 665
QY	121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGCACACACAATGTGAGCGTCTTTTGCCCTG 180
DB	TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGCACACACAATGTGAGCGTCTTTTGCCCTG 725

QY	181	AAACGAGACACACGACATCTCTCTCTCCTACTTTCATATATAGAAACCATCAAAAG	240
Db	726	AAACGAGACACACGACATCTCTCTCTCCTACTTTCATATATAGATGACAACTTAAG	785
QY	241	GAGAGAAA	248
Db	786	GATAAAGA	793
RESULT 12			
AAZ34785			
ID	AAZ34785 standard; cDNA; 1080 BP.		
XX			
AC	AAZ34785;		
XX			
DT	15-FEB-2000 (first entry)		
XX			
DE	Cat CD86 (B7-2) cDNA.		
XX			
KN	CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;		
KN	PTV; feline leukaemia virus; feline infectious peritonitis virus;		
KN	feline panleukopenia virus; feline calicivirus; feline reovirus-3;		
KN	feline sarcoravirus; feline coronavirus; feline syncytial virus;		
KN	feline sacroca virus; feline herpesvirus; feline Borna disease;		
KN	rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;		
KN	parasite; autoimmune disease; transplant rejection; therapy; ss.		
XX			
OS	Felis domesticus.		
XX			
FH	Key Location/Qualifiers		
FT	CDS	63..1055	
FT	/*tag= a		
PN	W09957271-A2.		
PD			
11-NOV-1999.			
30-APR-1999;	99WO-US09502.		
01-MAY-1998;	98US-0071699.		
(TEXA) TEXAS A & M SYSTEM.			
Collison EW, Hash SM, Choi I;			
MP1: 2000-052972/04.			
P-PSDB; AAY32278.			
Novel feline proteins used to produce feline vaccines which prevent			
infectious disease or to promote growth in homologous or heterologous			
species -			
Claim 6; Fig 3A; 186pp; English.			
<p>This is the nucleotide sequence of cDNA encoding feline CD86 (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of peripheral blood mononuclear cell mRNA and RACE-PCR. A vector comprising nucleic acid encoding feline CD86 ligand or feline soluble CD80 ligand is designated PST-2#19-2/011298 (ATCC 209821). The coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279) and a tumour antigen or an antigen from a pathogenic organism has the ability to activate or enhance activation of T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation of T-lymphocytes. The invention provides isolated nucleic acids encoding feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic acids, and polypeptides encoded by the nucleic acids. It also provides vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and further comprising immunogens derived from pathogens, especially feline immunodeficiency virus (FIV), feline leukaemia virus, feline infectious peritonitis virus, feline panleukopenia virus,</p>			


```
AC AA227931;
XX
XX 20-DEC-1999 (first entry)
XX
XX
DE Feline B7-2 protein coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX P-PSDB; AA41079.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 123-124; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;
XX
Query Match 63.3%; Score 227.2; DB 20; Length 996;
Best Local Similarity 94.8%; Pred. No. 2.8e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60.
XX |||||||
DB 484 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 543
XX
XX 61 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 120
XX |||||||
DB 544 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 603
XX
XX 121 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
XX |||||||
DB 604 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAAATGTGAGCGCTTTTGTGCCCTG 663
XX
XX 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 240
XX |||||||
DB 664 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 723
XX
XX 241 GAGAGAAA 248
XX |||||
DB 724 GATTAAGA 731
XX
RESULT 10
AA227932/c
ID AA227932 standard; DNA; 996 BP.
```

```
XX
XX AA227932;
XX
XX 20-DEC-1999 (first entry)
XX
XX
XX Complementary strand of feline B7-2 coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 124-125; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;
XX
Query Match 63.3%; Score 227.2; DB 20; Length 996;
Best Local Similarity 94.8%; Pred. No. 2.8e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
XX |||||||
DB 513 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 454
XX
XX 61 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 120
XX |||||||
DB 453 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 394
XX
XX 121 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
XX |||||||
DB 393 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAAATGTGAGCGCTTTTGTGCCCTG 334
XX
XX 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 240
XX |||||||
DB 333 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 274
XX
XX 241 GAGAGAAA 248
XX |||||
DB 273 GATTAAGA 266
XX
RESULT 11
AA234838
ID AA234838 standard; cDNA; 1080 BP.
```

```
XX 20-DEC-1999 (first entry)
DT
XX
DE Feline B7-2 protein (larger fragment) encoding DNA.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Fells catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX P-PSDB; AA41080.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases
XX
XX Claim 1: Page 125-126; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
SQ Sequence 509 BP; 170 A; 109 C; 106 G; 124 T; 0 other;
Query Match 63.3%; Score 227.2; DB 20; Length 509;
Best Local Similarity 94.8%; Pred. No. 2.2e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 1 ATCAAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTTCACT 60
DB 1 ATCAAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTTCACT 60
OY 61 ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTGACAGAACTGTACAACTTT 120
DB 61 ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTGACAGAACTGTACAACTTT 120
OY 121 TCATATGAGTTCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
DB 121 TCATATGAGTTCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
OY 181 AAACGTGAGACACTGAGAGATGCTCTCCCTACCTTTCAATATAGAAACCATCAAAAGG 240
DB 181 AAACGTGAGACACTGAGAGATGCTCTCCCTACCTTTCAATATAGAAACCATCAAAAGG 240
OY 241 GAGAGAAA 248
DB 241 GATTAAGA 248
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```
RESULT 8
AA227934/C
ID AA227934 standard; DNA; 509 BP.
XX
```

```
AC AA227934;
XX
XX 20-DEC-1999 (first entry)
DT
XX
DE Feline B7-2 gene (larger fragment) complementary DNA sequence.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Fells catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases
XX
XX Claim 1: Page 127; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
SQ Sequence 509 BP; 124 A; 106 C; 109 G; 170 T; 0 other;
Query Match 63.3%; Score 227.2; DB 20; Length 509;
Best Local Similarity 94.8%; Pred. No. 2.2e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 1 ATCAAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTTCACT 60
DB 509 ATCAAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTTCACT 450
OY 61 ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTGACAGAACTGTACAACTTT 120
DB 449 ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTGACAGAACTGTACAACTTT 390
OY 121 TCATATGAGTTCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
DB 389 TCATATGAGTTCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 330
OY 181 AAACGTGAGACACTGAGAGATGCTCTCCCTACCTTTCAATATAGAAACCATCAAAAGG 240
DB 329 AAACGTGAGACACTGAGAGATGCTCTCCCTACCTTTCAATATAGAAACCATCAAAAGG 270
OY 241 GAGAGAAA 248
DB 269 GATTAAGA 262
```

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RESULT 9
AA227931
ID AA227931 standard; DNA; 996 BP.
XX
```

OS Canis familiaris.
XX
KM WO9947558-A2.
PN
XX 23-SEP-1999.
PD
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
DR P-PSDB: AAY41078.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 109-111; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;
XX
Query Match 75.5%; Score 271; DB 20; Length 1795;
Best Local Similarity 86.6%; Pred. No. 3.9e-70;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
XX
QY 1 ATACAAGGTTACCCAGAACTAAGAGATGATTTTTCAGCTAACACTGAGAAATTCACCT 60
DB 487 ATACAAGGTTACCCAGAACTAAGAGATGATTTTTCAGCTAACAAACCGAATTCACAGT 546
XX
QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATATGACAGACAGTGTACAGCTT 120
DB 547 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATATGACAGACAGTGTACAGCTT 606
XX
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACATGTGAGCGTCTTTTGCCCTG 180
DB 607 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACATGTGAGCATCTTCTGTGCTCG 666
XX
QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCAATCAAAAG 240
DB 667 CAACCTGAGTCAAT--GAAGCTTCCCTCCCTACCTTCAATATAGAAACCAATCAAAAGTG 723
XX
QY 241 GAGAGAAAAGAGACAAACAGACCAAGAGATACATCCAGCTGAGAGATCT 300
DB 724 GAGAGAAAAGAGAGAGACAGACCAAGAGATGACGTCATATAGAAACCAAGATCT 783
XX
QY 301 GATGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGCGCAAAAGTACTACACA 359
DB 784 GATGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGCGCAACAGTACTACACA 842
XX
RESULT 6
AA27922/c
ID AA27922 standard; DNA; 1795 BP.
XX
AC AA27922;
XX
XX 2Q-DEC-1999 (first entry)
DT
XX
DE Canine B7-2S gene complementary DNA sequence.

XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 112-114; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;
XX
Query Match 75.5%; Score 271; DB 20; Length 1795;
Best Local Similarity 86.6%; Pred. No. 3.9e-70;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
XX
QY 1 ATACAAGGTTACCCAGAACTAAGAGATGATTTTTCAGCTAACACTGAGAAATTCACCT 60
DB 1309 ATACAAGGTTACCCAGAACTAAGAGATGATTTTTCAGCTAACAAACCGAATTCACAGT 1250
XX
QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATATGACAGACAGTGTACAGCTT 120
DB 1249 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATATGACAGACAGTGTACAGCTT 1190
XX
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACATGTGAGCGTCTTTTGCCCTG 180
DB 1189 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACATGTGAGCATCTTCTGTGCTCG 1130
XX
QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCAATCAAAAG 240
DB 1189 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACATGTGAGCATCTTCTGTGCTCG 1130
XX
QY 241 GAGAGAAAAGAGACAAACAGACCAAGAGATACATCCAGCTGAGAGATCT 300
DB 1072 GAGAGAAAAGAGAGAGACAGACCAAGAGATGACGTCATATAGAAACCAAGATCT 1013
XX
QY 301 GATGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGCGCAAAAGTACTACACA 359
DB 1012 GATGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGCGCAACAGTACTACACA 954
XX
RESULT 7
AA27933
ID AA27933 standard; DNA; 509 BP.
XX
AC AA27933;

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1, Page 127-128; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 359 BP; 128 A; 79 C; 69 G; 83 T; 0 other:

Query Match 100.0%; Score 359; DB 20; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
DB 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60

QY 61 ACTAAGTATGATGCTGCTCATGTAAGAAATCTCAAAATATGTGACAGACGTACAAAGTT 120
DB 61 ACTAAGTATGATGCTGCTCATGTAAGAAATCTCAAAATATGTGACAGACGTACAAAGTT 120

QY 121 TCTATCAGCTTGCCCTTTTCACTCCCTGAAGACACAATGTGAGCGCTTTTGTGCCCTG 180
DB 121 TCTATCAGCTTGCCCTTTTCACTCCCTGAAGACACAATGTGAGCGCTTTTGTGCCCTG 180

QY 181 AAACCTGAGACACTGAGATGCTGCTGCCCTTCACTTCAATATGAAACCATCAAAAGG 240
DB 181 AAACCTGAGACACTGAGATGCTGCTGCCCTTCACTTCAATATGAAACCATCAAAAGG 240

QY 241 GAGAGAAAAGAGACAAACAGACAGAGAGTACATACCAAGTACCTGAGAGATCT 300
DB 241 GAGAGAAAAGAGACAAACAGACAGAGAGTACATACCAAGTACCTGAGAGATCT 300

QY 301 GATGAAGCCGAGTGTATTAACATTTTGAAGACAGCTCAGCGGACAAAGTACTACACA 359
DB 301 GATGAAGCCGAGTGTATTAACATTTTGAAGACAGCTCAGCGGACAAAGTACTACACA 359

RESULT 2
AA27936/c
ID AA27936 standard; DNA; 359 BP.

XX AA27936;
XX
DT 20-DEC-1999 (first entry)

XX Feline B7-2 gene (smaller fragment) complementary DNA sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

XX allergic reaction; infectious disease; tumor development; feline;

XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Felis catus.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

PT treating, e.g. autoimmune and atopic diseases

XX Claim 1, Page 129; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 359 BP; 83 A; 69 C; 79 G; 128 T; 0 other:

Query Match 100.0%; Score 359; DB 20; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
DB 359 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 300

QY 61 ACTAAGTATGATGCTGCTCATGTAAGAAATCTCAAAATATGTGACAGACGTACAAAGTT 120
DB 299 ACTAAGTATGATGCTGCTCATGTAAGAAATCTCAAAATATGTGACAGACGTACAAAGTT 240

QY 121 TCTATCAGCTTGCCCTTTTCACTCCCTGAAGACACAATGTGAGCGCTTTTGTGCCCTG 180
DB 239 TCTATCAGCTTGCCCTTTTCACTCCCTGAAGACACAATGTGAGCGCTTTTGTGCCCTG 180

QY 181 AAACCTGAGACACTGAGATGCTGCTGCCCTTCACTTCAATATGAAACCATCAAAAGG 240
DB 179 AAACCTGAGACACTGAGATGCTGCTGCCCTTCACTTCAATATGAAACCATCAAAAGG 120

QY 241 GAGAGAAAAGAGACAAACAGACAGAGAGTACATACCAAGTACCTGAGAGATCT 300
DB 119 GAGAGAAAAGAGACAAACAGACAGAGAGTACATACCAAGTACCTGAGAGATCT 60

QY 301 GATGAAGCCGAGTGTATTAACATTTTGAAGACAGCTCAGCGGACAAAGTACTACACA 359
DB 59 GATGAAGCCGAGTGTATTAACATTTTGAAGACAGCTCAGCGGACAAAGTACTACACA 1

RESULT 3
AA27923
ID AA27923 standard; DNA; 840 BP.

XX AA27923;
XX
DT 20-DEC-1999 (first entry)

XX Canine B7-2S protein coding sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

XX allergic reaction; infectious disease; tumor development; canine;

XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Canis familiaris.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 54.2731 Seconds
(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccagacc.....ggcgacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N.GeneSeq_032802.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
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9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	359	20	AAZ27935
c	359	100.0	359	20	AAZ27936
3	271	75.5	840	20	AAZ27923
c	4	271	75.5	20	AAZ27924
5	271	75.5	1795	20	AAZ27921
c	6	271	75.5	20	AAZ27922
7	227.2	63.3	509	20	AAZ27933
c	8	227.2	63.3	20	AAZ27934
9	227.2	63.3	996	20	AAZ27931

c	10	227.2	63.3	996	20	AAZ27932	Complementary strA
c	11	227.2	63.3	1080	21	AAZ34838	Feline CD86 (B7-2)
c	12	227.2	63.3	1080	21	AAZ34785	Cat CD86 (B7-2) cd
c	13	227.2	63.3	2830	20	AAZ27929	Feline B7-2 protei
c	14	227.2	63.3	2830	20	AAZ27930	Feline B7-2 gene c
c	15	169.4	47.2	987	20	AAZ27915	Canine B7-2 protei
c	16	169.4	47.2	987	20	AAZ27916	Complementary strA
c	17	169.4	47.2	1897	20	AAZ27914	Canine B7-2 gene c
c	18	169.4	47.2	1897	20	AAZ27914	Pig costimulatory
c	19	124.6	34.7	1050	21	AAA49661	Human B lymphocyte
c	20	110	30.6	306	18	AAZ49198	Human B7-2 constan
c	21	110	30.6	306	21	AAZ49198	Human B7-2 extrac
c	22	110	30.6	738	20	AAZ80293	Nucleotide sequenc
c	23	110	30.6	738	22	AAZ89731	Chimeric human/po
c	24	110	30.6	764	18	AAZ62939	DNA encoding CD86
c	25	110	30.6	831	19	AAV03230	B7-2 cDNA. Homo s
c	26	110	30.6	972	20	AAV63208	Human co-stimulat
c	27	110	30.6	972	24	AAZ25510	Human B lymphocyte
c	28	110	30.6	1120	16	AAZ81351	Human B lymphocyte
c	29	110	30.6	1120	18	AAZ49181	Human B lymphocyte
c	30	110	30.6	1120	20	AAV5764	Human B7-2 antigen
c	31	110	30.6	1120	21	AAZ49181	Human B7-2 cDNA.
c	32	110	30.6	1424	21	AAZ29321	B70 type B antigen
c	33	110	30.6	1428	16	AAZ85873	Human cervical can
c	34	110	30.6	2205	22	AAH72616	Borrelia burgdorfe
c	35	78	21.7	210	16	AAZ01038	Drosophila melanog
c	36	77.2	21.5	1151	20	AAV55785	Human immune syste
c	37	77.2	21.5	1163	16	AAZ81366	Mouse B lymphocyte
c	38	77.2	21.5	1163	18	AAZ19182	Mouse B lymphocyte
c	39	77.2	21.5	1163	21	AAZ84050	Murine B lymphocyt
c	40	77.2	21.5	1261	16	AAZ01046	Mouse B7-2 exons m
c	41	66	18.4	942	19	AAZ9926	Rat CD86 coding se
c	42	36.8	10.3	1030	20	AAZ20338	Borrelia burgdorfe
c	43	36	10.0	1309	20	AAZ03323	Drosophila melanog
c	44	35.4	9.9	15306	23	ABL15764	Human immune syste
c	45	34.6	9.6	11726	24	ABL34063	Human immune syste

ALIGNMENTS

AAZ27935	standard: DNA; 359 BP.
ID	AAZ27935
AC	AAZ27935;
XX	20-DEC-1999 (first entry)
DT	
XX	Feline B7-2 protein (smaller fragment) encoding DNA.
DE	
KM	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW	allergic reaction; infectious disease; tumor development; feline;
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX	
OS	Felis catus.
XX	
PN	W09947558-A2.
PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06187.
XX	
PR	19-MAR-1998; 98US-0078765.
PR	17-APR-1998; 98US-0062597.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Sellins KS;
DR	WPI: 1999-571822/48.
DR	P-PSDB; AA41081.
XX	

LOCUS	BE823527	553 bp	mRNA	linear	EST 24-MAY-2001			
DEFINITION	GM700021A10F4 Gm-r1070 Glycine max cDNA clone Gm-r1070-8311 3', mRNA sequence.							
ACCESSION	BE823527							
VERSION	BE823527.1	GI:10255712						
KEYWORDS	EST.							
SOURCE	soybean.							
ORGANISM	Glycine max							
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.							
REFERENCE	1 (bases 1 to 553)							
AUTHORS	Vodkin, L., Kelm, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V., Repelding, J., Raph, C., Shoop, E., Pardini, J., Liu, L., and Lewin, H.							
TITLE	A functional genomics Program for Soybean (NSF 9872565)							
JOURNAL	Unpublished (1999)							
COMMENT	Other ESTs: AW508748 corresponding to Gm-r1030-965 (5')							

FEATURES

Source

```

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-r1070-8311"
/clone_lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked
set of 9,216 clones selected from cDNA libraries from
various tissues and stages of development of soybean that
represent 2,639 sequences from immature cotyledons, 1,770
from immature seed coats, 3,938 from flowers, and 869
from young pods. The 5' ESTs of the source clones from
the different libraries was used to select singletons, or
a representative of each contig, which were reracked to
form library Gm-r1070. The cDNA clones of the reracked
Gm-r1070 library were then sequenced at the 3' end. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Reizel, Center for Computational
Genomics and Bioinformatics, University of Minnesota,
http://www.cbc.umn.edu/ResearchProjects/Soybean/Index.html
. Reracking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and 3' sequencing by the
Reck Center for Comparative and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/reck.html. Note: The
corresponding 5' EST from each clone in the Gm-r1070
library is listed in the 'OTHER EST' field. The detailed
information on the source library for each clone can also
be obtained by referring to the Genome Systems clone ID of
the original cDNA library that is also listed under
'OTHER EST'."

```

Query March	10.8%	Score 38.6;	DB 10,	Length 553;
Best Local Similarity	51.4%;	Pred.No. 37;		
Matches 89;	Conservative	0;	Mismatches 84;	Indels 0;
			Gaps	0;
145-CCCTAAGCAGACATGTGAGCGCTTTTGTGTGGCCGGAACCTGAGACACGTGGATGCTG	204			

```

Db 166 CCAGAGGAGAGAAATGTGATGTGATAGAGGCGCTGACCAACAAAAAATACTAGTAGTG 2253
QY 205 CTCTCCCTACCTTTCAATATATGAAACCATCAAAAGGAGAGAAAGACGCAACAGACC 2645
      |||||      |||
Db 226 TCTCTCCCTCTCTCTCCATCAAAACCTTTTGCAAAAGGATATGAGATGAGCAAGACC 2853
      |||||      |||
QY 265 AACGAAGAAGTACCATACCACTACTCTGAGACGATCTGATGTAAGCCCACTGATAT 317
      ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 AACTGAGAGAAACACCACCAAGTAGAGCGGCTCCACTGTGTGATGACACTGTAT 338
      ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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Search completed: October 20, 2002, 04:30:18
Job time : 435.863 secs
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	Matches	75; Conservative	0; Mismatches	57; Indels	0; Gaps	0;
OY	228	AACCATTAAGGAGAGAAAAAGAGACCAACACAGCAAGAAAGACTACCATTCACGCT	287			
Db	464	AAACAAACACAGGAGGAGAAAAAAGAGCGGAAACGACTAACAGAGAAACAAACACACACAA	523			
OY	288	ACCTGACAGATCTGATGAAGACCCAGTGTATTAACTTTTGAAGACAGCTTCAGGCGACAA	347			
Db	524	AGCGGAAAAAACACACAAAAAAGAGCAATTACAAAGAACAAACAAACACACACCGGAGAA	583			
OY	348	AAAGTACTACACA	359			
Db	584	AAAGAAAAAGCA	595			

RESULT 13	AA973397/c	LOCUS	DEFINITION
AA973397	378 bp	linear	EST 17-JUN-1998
004404.s1	NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1569006 3'		
	similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN		
CD86	PRECURSOR ; mRNA sequence.		

ACCESSION	AA973397	
VERSION	AA973397.1	GI:3148577
KEYWORDS	EST.	
SOURCE	human.	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 378)

JOURNAL COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LNL at:
www.Dio.lnl.gov/bbrp/image/image.html
Insert length: 501
Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES	Location/Qualifiers
source	1. .378

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1569006"
/clone_lib="NCI-CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT733 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonalido. "

```

	Query Match	11.3%	Score 40.4	DB 9	Length 378
	Best Local Similarity	81.1%	Pred. No. 14		
	Matches 60	Conservative 0	Mismatches 11	Indels 3	Gaps 1
QY	287	TACCTGAGANCTGATGTGAAGCCCGT---	TATTACATTTTGAAGACGCTCAGGGC	343	
DB	375	TACCTGAAGATTTGATGTGAAGCCCGCTGTTTT	TAATAAGTTCGAAGACATCTTCATGGC	316	
QY	344	ACAAAGTACTACAA	357		

Db 315 ACAAAAGTGATACA 302

RESULT 14				
TA254E04P/C				
LOCUS	TA254E04P	538 bp	DNA	linear
DEFINITION	T. brucei sheared genomic DNA clone 254e04, forward sequence, genomic survey sequence.			

ACCESSION	AL482448
VERSION	AL482448.1
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei.

ORGANISM *Trypanosoma brucei*
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae
Trypanosoma.

REFERENCE
 (1) (bases 1 to 538)
 AUTHORS
 Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S. E., Rajandream, M. A. and Barrell, B. G.

JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUT8 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES	Location/Qualifiers
source	1. .538

BASE COUNT	127 a	117 c	62 g	232 t
ORIGIN				

Query Match	10.9%;	Score 39;	DB 12;	Length 538;
Best Local Similarity	47.1%;	Pred. No. 30;		
Matches 120; Conservative	0;	Mismatches 135;	Indels 0;	Gaps 0;

77 TCATGAGNAATCTCAAAATAATGTCACAGAACTGTACAAAGTTTCTATCAGCTTGCCTT 13

Db 385 TCAGTAATTCATCTGGTATGACTGAACCAATAAGAAATTTATTATTATTACATT 32

137 TTTCAATCCCTGAAGCACACACATGTGAGCGCTTTTGTGCCCTGAACCTGGAGACACATGG 19

Db 325 TTGCAGAGGTGAAACGAAATAAGTGGAGCACTTTGGTTTCATGATGGTGCAGTGAACGAG 26

197 AGATGCTCTCCCTACCTTCATATGAAACCATCAAAAGGAGAGAAAGAGACA 25

257 AACAGAACCAAGAGGTATCCATACCAAGTACCTCGAGAGATCGATGAAGCCAGTGA 311
DB AACAGCCCAACCAAGGTACAGAACAGCAACAGAGCGGTATACAGAAAGAAAAAAGGAACG 20

Db 205 A A A G G A A A A G G A G A G A A A A G A A A C A C A T C A G T G G A G A A C C G A T G A T A 14

317 TTACATTTTGAGA 331

Db 145 ATGGGATTGAAA 131

RESULT 15
BE823527


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VERSION      BF064222.1  GI:10823132
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 543)
AUTHORS      NCJ-CGAP http://www.ncbi.nlm.nih.gov/ncjgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
JOURNAL      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: -40UP from Gluco
              High quality sequence stop: 496.
FEATURES
SOURCE
1..543
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    /db_xref="taxon:9606"
    /clone="IMAGE:3390507"
    /clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
    /lab_host="DH10B"
    /note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with
    a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
    Equal amounts of plasmid DNA from five normalized
    libraries were mixed, and ss circles were made in vitro.
    Following HAP purification, this DNA was used as tracer in
    a subtractive hybridization reaction. The driver was
    PCR-amplified cDNAs from pools of 5,000 clones made from
    the same 5 libraries. The pools consisted of the following
    libraries and clones: Soares NBHSF pool 1:
    309384-310919, 323208-325895 Soares NB2HP pool 1:
    145032-147335, 147720-148103, 148873-149255, 15002 -
    150407, 151176-152327 Soares NB2HF-9W pool 1:
    758280-760583, 772104-774407 Soares NB4PA pool 1:
    304776-306311, 320136-322823, 326280-326663 Soares NB4OT
    pool 1: 723720-726407, 739080-740999 Subtraction by Benito
    Soares and M. Fatima Bonalito."
BASE COUNT   151 a 104 c 112 g 175 t 1 others
ORIGIN
Query Match      21.3%; Score 76.4; DB 10; Length 543;
Best Local Similarity 70.5%; Pred. No. 5,2e-08;
Matches 117; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
OY 195 GGAATGCTCTCTCTCCCTCAATRTAGAAACCATCAAAAGGAGGAGAAAAGAG 254
      1 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 466 GAAAGACGGCGCTCGACACTTATTAATGTGGAACCAACCAATGGAGGGAGAAAGAG 407
      1 111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 255 CAAACAGACCAAGGAAGTAGTACCTACACAGCTGAGAGATCTGATTAACCCGATG 314
      1111111 111111 11111 111 111111 11111111 11111 11111
Db 406 TGAACAGACCAAGGAAGAGAAAAATCCATATACCTGAAAGATCTGATGAACCCAGCG 347
      1111111 111111 11111 111 111111 11111111 11111 11111
OY 315 ---ATTATACATTTTGAAGACAGCCCGAGGAGCAAAAAGTACTCTCA 357
      11111 11111 111111 111 11111111 11111 11111 11111
Db 346 TGTTTTAAAGTTCAAGACATCTTCATCGACAAAGGATGATCA 301
      11111 11111 11111 111 11111111 11111 11111 11111
RESULT 7
A1750143/c A1750143 480 bp mRNA linear EST 22-JUN-1999
DEFINITION at27h10.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2356587 3' similar to SW:CB86.HUMAN P42081 T LYMPHOCYTE
ACTIVATION ANTIGEN CD86 PRECURSOR.; mRNA sequence.
ACCESSION A1750143
VERSION A1750143.1 GI:5128407
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

[illegible]

Db	328	TGTTTTAAAGTTCGAACATCTTCATGGCAGCAAAAAGTGATACA	373
RESULT 4			
LOCUS	A1093604/c	570 bp	mRNA
DEFINITION	cou82B09.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1634497 3' similar to SW:CD86.HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR , mRNA sequence.		EST 10-NOV-1998
ACCESSION	A1093604		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	1 (bases 1 to 570)		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapdb@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 801 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amershams High quality sequence stop: 400.		
FEATURES	Location/Qualifiers		
Source	1..570		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"		
	/note="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 1450382-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF-9W pool 1: 778280, 760583, 772104-774407 Soares NBdPA pool 1: 304776-306311, 320136-322823, 326280-326563 Soares NBHOT pool 1: 73720-726407, 735080-740999 Subtraction by Benton Soares and M. Fatima Bonaldo."		
BASE COUNT	150 a 107 g 134 c 179 t		
ORIGIN			
Query Match	21.5%:	Score 77.2:	DB 9: Length 570;
Best Local Similarity	73.4%:	Pred. No. 3.4e-08:	
Matches 113; Conservative	0: Mismatches 38; Indels 3; Gaps 1;		
QY	207 CTCCTACTTTCCATATAGAACCATCAAAAAGGAGAGAAAAAGAGCAACAGACACAA	266	
Db	452 CTCGCACCTCTTAATAATGTGAACCAACACATGAGGAGGAGATGATGACAGACAA	393	
QY	267 CGAAGAGTACCTTACCACTGCCGAGTACGAGATGATCAACCCACAG--TATTACAT	323	
Db	392 GAAGAAGGAAAAATCATATACCTGGAAGATGATGATAAACCCAGCGTCTTTTAAAG	333	
QY	324 TTGGAAGACAGCCTCAGGCGACAAAAGTAGTACACA	357	
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RESULT 5			
AA946810/c			

LOCUS	AA946810	504 bp	MRNA	linear	EST 23-JUL-1998
DEFINITION	0433c01.s1 NCI CGAP Kid5 Homo sapiens CDNA clone IMAGE:1589088 3'				
ACCESSION	CD86 PRECURSOR				
VERSION	AA946810.1	GI:3110205			
KEYWORDS	EST.				
ORGANISM	Homo sapiens				
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 504)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.G.E. Consortium/BLNT at: www-bio.llnl.gov/dbfp/image/image.html Insert length: 1276 Std Error: 0.00 Seq primer: -40ml3 fwd. E7 from Amersham High quality sequence stop: 457.				
FEATURES	Location/Qualifiers				
SOURCE	1..504 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1589088" /clone_1id="NCI CGAP Kid5" /tissue_type="2 pooled tumors (clear cell type)" /lab_host="DH10B" /note="organ: kidney; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' AACGTGAGAAATTCGCGCGCAATATTTTATTTTATTTT 3'], AACGTGAGAAATTCGCGCGCAATATTTTATTTTATTTT 3'], (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."				
BASE COUNT	136 a 94 c 109 g 165 t				
ORIGIN					
Query Match	21.3%;	Score 76.4;	DB 9;	Length 504;	
Best Local Similarity	70.5%;	Pred. No. 5.2e-08;			
Matches 117; Conservative	0;	Mismatches 46;	Indels 3;	Gaps 1;	
OY	195 GGAATGCTCTCTGCTCCCTCACTTTCAATATATGAAACCATCAAGAGGAGGAGAAAGAGAG 254				
DB	472 GAGAGAGCGGCGCTCGCAACTCTTATTAATATGTGGAAACACACCAATGAGGAGGAAGAGG 413				
OY	255 CAAAGACACCAAGAAAGAGTACCATACACGATCTGAGATCTGATGATGAAGCCAGTGG 314				
DB	412 TGAACAGACCCAAAGAAAGAGAAATATCCATATACCTGAAAGATCTGATTAACCCAGCG 353				
OY	315 ---TATTAACATTTTGAAGACGCTCGAGGCGACAAAGACTACCA 357				
DB	352 TGTTTTAAAGTTGCAAGACATCTTCATGCGACAAAGATGATACA 307				
RESULT 6	BF064222/c	543 bp	MRNA	linear	EST 16-OCT-2000
LOCUS	BF064222				
DEFINITION	7157B02.x1 Soares NSF.E8.9W.CT.PA.P.S1 Homo sapiens CDNA clone IMAGE:3390507 3'				
ACTIVATION	ANTIGEN CD86 PRECURSOR				
ACCESSION	BF064222				

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 427.863 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmoy:*
- 5: em_estmoy:*
- 6: em_estmoy:*
- 7: em_estmoy:*
- 8: em_estmoy:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_est3:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104.8	29.2	512	9	AA056905 EST224F P
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3	78	21.7	496	9	AW516826 xq04h01.x
4	77.2	21.5	570	9	AI093604 ou82b09.s
5	76.4	21.3	504	9	AA946810
6	76.4	21.3	543	10	BF064222
7	72.4	20.2	480	9	AT750143
8	64.8	18.1	347	10	BG001664 RC4-GN006
9	57.8	16.1	1002	10	BF137460 601780644
10	55.8	15.5	486	10	BI132458 AR03A11L
11	42.2	11.8	391	9	AT632116 ts85b01.x
12	40.8	11.4	858	10	BG252809 602365378
13	40.4	11.3	378	9	AA973397 o044a04.s
14	39	10.9	538	12	TA254E04P
15	38.6	10.8	553	10	BE823527 GM700021A
16	38.2	10.6	654	12	AZ233626 RPCI-23-9
17	38	10.6	565	9	BE118052 UT-R-B51-

18	37.8	10.5	692	9	AV723257	AV723257 AV723257
19	37.4	10.4	619	12	FR0004538	Z88321 F.rubripes
20	37.2	10.4	690	12	AZ220823	AZ220823 Sheared D
21	37	10.3	386	10	BE921966	BE921966 EST425755
22	37	10.3	484	10	BG511725	BG511725 sad42c05.
23	37	10.3	496	10	BG510033	BG510033 sad26g11.
24	37	10.3	512	12	AQ342188	AQ342188 RPCI11-12
25	37	10.3	679	10	BM406580	BM406580 EST580907
26	36.6	10.2	275	9	BE262554	BE262554 BA426183
27	36.6	10.2	760	10	BE262554	BE262554 601154211
28	36.4	10.1	294	12	AZ510008	AZ510008 1M0354P10
29	36.4	10.1	1041	12	CNS02BOY	AL190123 Tetradon
30	36	10.0	802	10	BG284658	BG284658 602408837
31	36	10.0	959	12	CNS06T7U	AL414208 T3 end of
32	35.4	9.9	599	9	AW966116	AW966116 EST378189
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34	35.2	9.8	612	12	BH186623	BH186623 031-E-08-
35	35.2	9.8	612	12	CNS07R27	AL623569 T3 end of
36	35.2	9.8	658	10	BE823320	BE823320 GM700020B
37	35.2	9.8	1101	12	CNS0141H	AL103583 Drosophila
38	35	9.7	385	9	AA358198	AA358198 EST67073
39	35	9.7	706	12	AQ855359	AQ855359 Cp61892B
40	34.8	9.7	402	9	AI381291	AI381291 tc49f03.x
41	34.8	9.7	451	9	AW020789	AW020789 df14d12.y
42	34.8	9.7	477	10	BI495304	BI495304 df116g07.
43	34.8	9.7	657	10	BE597274	BE597274 EST495952
44	34.8	9.7	703	10	BI495303	BI495303 df116g07.
45	34.8	9.7	783	10	BG934273	BG934273 SK1-0569

ALIGNMENTS

RESULT 1
LOCUS AA056905 512 bp mRNA linear EST 18-SEP-1996
DEFINITION EST224F Pig Spleen lambda gt 11 library (Clontech Cat # PL1006b)
Sus scrofa cDNA clone SPL224 forward similar to L25259 C11A4
Counter-receptor , human, mRNA sequence.

ACCESSION AA056905 GI:1549545
VERSION AA056905
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 512)
AUTHORS Tuglie,C.K., Wahls,S. and Schmitz,C.
TITLE Expressed Sequence Tags from Pig Spleen
JOURNAL Unpublished (1996)
COMMENT Contact: Tuglie CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ktuglie@iastate.edu

PCR Primers
FORWARD: TGCGCAGCTCCTG
BACKWARD: GACCGCGCTCAGCT
Insert length: 950 Std Error: 50.00
Seq primer: TGCGCAGCTCCTG.
Location/Qualifiers
1..512
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/clone="SPL224"
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/dev_stage="adult"
/note="Oligo (dT) primed"

BASE COUNT 125 a 106 c 114 g 163 t 4 others

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LOCUS	AX002781	738 bp	DNA	linear	PAT 21-AUG-2000
DEFINITION	Sequence 4 from Patent WO9855607.				
ACCESSION	AX002781				
VERSION	AX002781.1	GI:9885109			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct.				
REFERENCE	synthetic construct.				
AUTHORS	artificial sequence.				
TITLE	1 (bases 1 to 738)				
JOURNAL	Bebington, C.R. and Carroll, M.W.				
FEATURES	Vector				
source	Patent: WO 9855607-A 4 10-DEC-1998;				
	BEBINGTON CHRISTOPHER ROBERT (GB);				
	Carroll, M.W.				
	Location/Qualifiers				
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	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	1..>738				
	/note="unnamed protein product"				
	/codon_start=1				
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	SELAVFWQDENLVLNHYVLEKEFEDSVHSKYMRTSFSDSWTLRLNLIQKQGLY				
	QCILHHRKPTGMIRIHMNSLSVLANSEIPIINTEPNVYINLTCSSIHGYPPE				
	KMSVLLRTKSTIEYDGMOKSDQNTYELTDVSISSVSPDVTSMNTIICILETDK				
	TRLSSPFSIELEDPDPPHPIPGSGS"				
BASE COUNT	215 a	168 c	148 g	207 t	
ORIGIN					
Query Match	30.6%;	Score 110;	DB 6;	Length 738;	
Best Local Similarity	73.5%;	Pred. No. 3.7e-19;			
Matches 169;	Conservative	0;	Mismatches 55;	Indels 6;	Gaps 2;
QY	1	ATACAGGTTACCCGAAACCTAGAGATGTAATTTTCAGCTTAACACGTGAGATTTCAACT	60		
Db	460	ATACAGGTTACCCGAAACCTAGAGATGTAATTTTCAGCTTAACACGTGAGATTTCAACT	519		
QY	61	ACTAGTATGATACGTCATGTAAGAAATCTCAAAATTAATGAGACAGACTGACAGCGTT	120		
Db	520	ATCGAGTATGATGTAATTAATGACAGAAATCTCAAGATAATATGTCACAGAACTGTACAGCGTT	579		
QY	121	TCTATCAGCTTGCCCTTTTTCAGTCCCTGAG--CACACAATGTGAGCGTCTTTTGTCGC	177		
Db	580	TTCATCAGCTTGCTGCTTTTTCATCCCTGATGTAAGACCAATATGACCATCTTCTGTAAT	639		
QY	178	CTGAACCTGAGACACTGAGATGCTGCTTCCTCCTACCTTTCAATATAGA	227		
Db	640	CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACTTCTCTATAGA	686		
RESULT 13					
AX149548	AX149548	738 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX149548	738 bp	DNA	linear	PAT 08-JUN-2001
DEFINITION	Sequence 9 from Patent WO0136486.				
ACCESSION	AX149548				
VERSION	AX149548.1	GI:14347987			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct.				
REFERENCE	synthetic construct				
AUTHORS	artificial sequence.				
TITLE	1 (bases 1 to 738)				
JOURNAL	Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W.,				
FEATURES	Ellard, F.M. and Myers, K.A.				
source	Antibodies				
	Patent: WO 0136486-A 9 25-MAY-2001;				
	Oxford Biomedica (UK) Limited (GB)				
	Location/Qualifiers				
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BASE COUNT	215 a	168 c	148 g	207 t
ORIGIN	/note="B7-2.514.1"			
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Best Local Similarity	73.5%: Pred. No. 3.7e-19;			
Matches 169; Conservative	0; Mismatches 55; Indels 6; Gaps 2;			
QY	1 ATACAGGTTACCCGAGACCTAAGAGATGATTTTCAGCTAAACATGAGAAATCAACT 60			
Db	460 ATACACGGTTACCCGAGACCTAAGAGATGATTTTCAGCTAAACCAAGAAATCAACT 519			
QY	61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTCAGCAAACTGTACACGTT 120			
Db	520 ATCGAGTATGATGATTAATGAGAAATCTCAAGATTAATGTCACAGAACTGTACACGTT 579			
QY	121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAG--CACAAATGTAGAGGCTTTGTGCC 177			
Db	580 TCCATCAGCTTGCCTTTTTCAGTCCCTGAG--CACAAATGTAGAGGCTTTGTGTATT 639			
QY	178 CTGAACATGAGAGACACTGAGATGCTGCTCCCTACCTTCATATATAGA 227			
Db	640 CTGGAACACTGACA--AGACCGGCGCTTTTATCTTACCTTCTCTATAGA 686			
RESULT 14				
LOCUS	ARI47737	751 bp		DNA
DEFINITION	Sequence 34 from patent US 6225042.			
ACCESSION	ARI47737			
VERSION	ARI47737.1	GI:15111827		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 751)			
TITLE	Cal, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P. A.			
JOURNAL	Antigen presenting system and methods for activation of T-cells			
FEATURES	Patent: US 6225042-A 34 01-MAY-2001;			
source	Location/Qualifiers			
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ORIGIN	/organism="unknown"			
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Best Local Similarity	73.5%: Pred. No. 3.7e-19;			
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QY	1 ATACAGGTTACCCGAGACCTAAGAGATGATTTTCAGCTAAACATGAGAAATCAACT 60			
Db	484 ATACACGGTTACCCGAGACCTAAGAGATGATTTTCAGCTAAACCAAGAAATCAACT 543			
QY	61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTCAGCAAACTGTACACGTT 120			
Db	544 ATCGAGTATGATGATTAATGAGAAATCTCAAGATTAATGTCACAGAACTGTACACGTT 603			
QY	121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAG--CACAAATGTAGAGGCTTTGTGCC 177			
Db	604 TCCATCAGCTTGCCTTTTTCAGTCCCTGAG--CACAAATGTAGAGGCTTTGTGTATT 663			
QY	178 CTGAACATGAGAGACACTGAGATGCTGCTCCCTACCTTCATATATAGA 227			
Db	664 CTGGAACACTGACA--AGACCGGCGCTTTTATCTTACCTTCTCTATAGA 710			
RESULT 15				
LOCUS	ARI59759	751 bp		DNA
DEFINITION	Sequence 34 from patent US 6251627.			
ACCESSION	ARI59759			
VERSION	ARI59759.1	GI:16222532		
KEYWORDS	.			


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BASE COUNT      302 a      241 c      202 g      249 t
ORIGIN
Query Match      34.7% ; Score 124.6 ; DB 6 ; Length 994 ;
Best Local Similarity 73.6% ; Pred. No. 4,4e-23 ;
Matches 173 ; Conservative 0 ; Mismatches 59 ; Indels 3 ; Gaps 1 ;

OY      1 ATACAGGTATCCCAAGCTAGAGATGATTTTCAGTCAACCAACTGATTAACCT 60
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      460 ACACAGGCTACCCAGAACCCAGAGATGATATGTGCTAATATACAGATTTCAAC 519
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      61 ACTAAGTGTGCTGCTGATGAGAAATCTCAAAATATGTGACAGACTGTCAACGTT 120
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OY      121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACACAAATGAGCGCTTTTGCCCTG 180
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DB      580 TCAATCAGAGGTGTCTCTTCCATCCCTCCGAGACAAATGTGAGCATCGTCTGTCTG 639
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OY      181 AAATGAGACACTGAGAGA---TCCTGCTCTCCCTACCTTCAATATAGAACCA 232
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DB      640 CAACCTGAGCCAGACAGACACTGCTTTTCTCCCTACCTTCAATATAGATGCAA 694
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10      164161 bp      DNA      linear      PRI 01-NOV-2001
LOCUS      AC068630
DEFINITION  Homo sapiens 3 BAC RP11-289N10 (Roswell Park Cancer Institute Human
ACCESSION  AC068630
VERSION    AC068630
KEYWORDS   complete sequence.
SOURCE     human.
ORGANISM   human.
REFERENCE  1 (bases 1 to 164161)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          Muzny D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C.,
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Taylor, T., Telirod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, Y., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlecczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 164161)
Worley, K.C.
Direct Submission
Submitted (06-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 164161)
Worley, K.C.
Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 1, 2001 this sequence version replaced gi:16152225.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT REPORT:

location/Qualifiers

FEATURES

source

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TITLE Cloning and distribution of cattle CD86
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 924)
AUTHORS Brooke, G.P.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2000) Brooke G.P., Cellular Immunology, Institute
For Animal Health, Compton, Berks, RG20 7NN, UNITED KINGDOM

FEATURES
Source
1. 924
/organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="monocyte"
/tissue_type="peripheral blood"
/dev_stage="adult"
/country="United Kingdom"
72. .924
/gene="CD86"
72. .>924
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/db_xref="GI:10803380"
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LPCHPMTOMLSDELVIEMQDNKILVLEFKGPKPNVNPVKYIGRTSPDSDMTL
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INLTCSSIDGYPEPORMYVSLNNTSSSTIDAVKKSQSIITELVNSISVSPRIPE
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LKKKKKRL"

gene
CD8
72. .>924
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LNVIFCALQLEPKIILSQPINIDAKSPVPDPDHILMIALLVVVSQWFLT
LKKKKKRL"

BASE COUNT 295 a 226 c 175 g 228 t
ORIGIN

Query Match 40.6%; Score 145.6; DB 4; Length 924;
Best Local Similarity 76.7%; Pred. No. 1e-28;
Matches 178; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 ATACAAGGTTACCCAGACATGAAGATGATTTTCACTAAGACAGTGAATTCACACT 60
DB 573 ATACAAGTTACCCAGACATGAAGATGATTTTCACTAAGACAGTGAATTCACACT 632
QY 61 ACTAAGTATGATCTGTCATGAAGAATCTCAAAATATGTCAGACAGTGTACAGCTT 120
DB 633 AGCACCATTGATGCTGTGATGAAGAAATCTCAAGTATATATACAGACATATACATGTT 692
QY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACATGTGAGCGCTTTTGTGCCCTG 180
DB 693 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACATGTGAGCGCTTTTGTGCCCTG 752
QY 181 AAACGTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGAACCA 232
DB 753 CAACCTGAGCCAGACAGATATTTATCCCACTTCAATATAGATGCA 804

RESULT 8
LOCUS PICCD86G 994 bp mRNA linear MAM 17-JUN-1997
DEFINITION Sus scrofa CD86 mRNA, complete cds.
ACCESSION L76099.1 GI:2198558
VERSION L76099.1 GI:2198558
KEYWORDS T cell costimulation.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Mahrer, S.E., Karmann, K., Min, W., Hughes, C.C., Pober, J.S. and
Bothwell, A.L.
Porcine endothelial CD86 is a major costimulator of xenogeneic
human T cells: cloning, sequencing, and functional expression in
human endothelial cells
JOURNAL J. Immunol. 157 (9), 3838-3844 (1996)
MEDLINE 97047772

COMMENT GSDB:S:74002
FEATURES
Source
1. 994
/organism="Sus scrofa"
/db_xref="taxon:9923"
/cell_line="PEC-A"
/cell_type="endothelial"
/clone_id="3"
/dev_stage="adult"
1. 994
/gene="CD86"
1. 978
/gene="CD86"
/standard_name="B7-2"
/note="putative"
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/db_xref="GI:2198559"
/translation="WGLSNILFVNYLLISGAASLKSQAVFNETGELEPCHFTNSQNL
DELVIFMODONLVLYELYRGOEKPHNNSRYMGRTSPDQATWTLRLHNVQIKGSI
OCFIIHKGPHGLVPIHOMSDLSLANSOPEINLTHNTENSVINLTCSSIDGYPEP
ORMVWMLNMTKNTSTEDADMKSSONNITELVNSISVSLPIPETNNSIVCLDLEPS
KLLSLPCNIDAKPPQPPVDPDHITLIALLVVYVCGSVFTLKRKKQPGPS
NCGETIKNRKASQTKNRKAEVHERSDADQDVNLLKTSADNSTDF"

3'UTR
polyA_site
/gene="CD86"
/note="putative"
994
/gene="CD86"
/evidence="experimental"
241 c 202 g 249 t

BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN

Query Match 34.7%; Score 124.6; DB 4; Length 994;
Best Local Similarity 73.6%; Pred. No. 4.4e-23;
Matches 173; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATACAAGTTACCCAGACATGAAGATGATTTTCACTAAGACAGTGAATTCACACT 60
DB 460 ACACAAGGTTACCCAGACATGAAGATGATTTTCACTAAGACAGTGAATTCACACT 519
QY 61 ACTAAGTATGATCTGTCATGAAGAATCTCAAAATATGTCAGACAGTGTACAGCTT 120
DB 520 ACTGAGCATATGCTGATGATGAAGAATCTCAAAATATGTCAGACAGTGTACAGCTT 579
QY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACATGTGAGCGCTTTTGTGCCCTG 180
DB 580 TCAATCAGGGGTCTCTTCCCATCCCTCCGAGACAAATGTGAGCATGTGTGCTGCTG 639
QY 181 AAACGTGAGACACTGAGGAGG---TGCTGCTCTCCCTACCTTCAATATAGAACCA 232
DB 640 CAACCTGAGCCAGACAGACAGTGTCTTCTCCCTACCTTCAATATAGATGCA 694

RESULT 9
LOCUS AX027016 994 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 13 from Patent WO0037102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Rogers, N.J., Dorling, A. and Lechler, R.I.
Immunosuppression
Patent: WO 0037102-A 13 29-JUN-2000;
LECHLER ROBERT IAN (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
location/Qualifiers
1. 994

PUBMED 11491535
 REFERENCE 2 (bases 1 to 901)
 AUTHORS Villinger,F.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory University School of Medicine, Winship Cancer Institute, 1365B Clifton Rd, Atlanta, GA 30322, USA
 FEATURES
 source 1..901
 /organism="Papio cynocephalus anubis"
 /sub_species="anubis"
 /db_xref="taxon:9555"
 sig_peptide 7..834
 CDS
 /note="B7.2"
 /product="CD86 protein precursor"
 /protein_id="AAK37532.1"
 /db_xref="GI:1364984"
 /translation="MGLSILFVAFLLSGAAPLIQAVENETADLPQFANSQNSRLSELVFMQENLVLNEYLGREKEDSVHSKMGRTSPESWTLRLNLIQIKKGLYOCIIHKRPQEMIRIHOVNSLSVLAISOPEIYISNITENMYINLCSIHGPEPEKMSVILRTKSTTEYDGYMOKSODNTETLDVSLISVSPDYTSNMWTLPCVLETKTOLLSPESTINMERESDQTKRKREKINVPERSDEAQCYFKSLKTPSCDKSDTHF"
 misc_feature 690
 /note="144 nucleotide insertion in Homo sapiens CD86"
 BASE COUNT 281 a 193 c 178 g 249 t
 ORIGIN
 Query Match 50.9%; Score 182.6; DB 9; Length 901;
 Best Local Similarity 74.5%; Pred. No. 1.2e-38;
 Matches 272; Conservative 0; Mismatches 84; Indels 9; Gaps 3;
 QY 1 ATCAAGTTTACCAGAACTTAAGAGATGATATTTTCACTGCTTAACAGTGAATTCACACT 60
 DB 466 ATACAGGTATACCCAGAACTGAGAGATGATGTTTCTTAAGAACCAAGATTCACACT 525
 QY 61 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGTAACAGTT 120
 DB 526 ATCGATGATGATGTTGTATGCAAAATCTCAAGATTAATGTCCACAGAACTGACAGCTT 585
 QY 121 TCTATGAGCTTGCTTTTTCAGTCCCTGAAG---CACACAAATGTGAGCGCTCTTTGTGCG 177
 DB 586 TCCATGAGCTTGCTTTTTCAGTCCCTGAAG---CACACAAATGTGAGCGCTCTTTGTGCG 177
 QY 178 CTGAAGCTGGAGACACTGAGATGCTGCTCCCTACTCTTCAATATAGAACCAATCAAA 237
 DB 646 CTGGAAGCTGACA---AGACACAGCTTTTATCTCTACCTTCTCTATGAGAACCAACACA 702
 QY 238 AGGAGAGAAAAAGAGACAAAGACCAAGAAAGATACATACCCAGCTACCTGAGAGA 297
 DB 703 ATGGAAGAGGAAAGAGATGACAGACCAAAAAAGAAATAATATATACCTGAAAGA 762
 QY 298 TCTGATGAGAGCCAGT---TATTAACATTTTGAAGACAGCCTCAGGCGACAAAAGTACT 354
 DB 763 TCTGATGAGAGCCAGTGTGTTTAAAGTTGAAGACACCTTCATGCGACAAAAGTGAT 822
 QY 355 ACACA 359
 DB 823 ACACA 827
 RESULT 6
 LOCUS AF106826 1897 bp mRNA linear MAM 14-DEC-1999
 DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
 ACCESSION AF106826
 VERSION AF106826.1 GI:6572516
 KEYWORDS
 ORGANISM
 dog.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 1897)
 AUTHORS Yang,S. and SIm,G.K.
 TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules
 JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
 MEDLINE 20039396
 REFERENCE 2 (bases 1 to 1897)
 AUTHORS Yang,S. and SIm,G.-K.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA
 FEATURES
 source 1..1897
 /organism="Canis familiaris"
 /db_xref="taxon:9615"
 /cell_type="peripheral blood mononuclear cells"
 gene 1..1897
 5'UTR 1..5
 CDS
 /gene="CD86"
 /function="counter-receptor for CD28 and CD152 (CTLA4)"
 /codon_start=1
 /product="B7-2 protein"
 /protein_id="AAE17297.1"
 /db_xref="GI:6572517"
 /translation="MYLRCTMELNLIFFVNTLLLYGASMSQAVFNKTELPCHFTN SONISIDELVLFEMQDDDKLYLVELYELVGRKKNPOVHKRKYSPDKMNTLRLNIQI KDKGLQCFYVHKRPGKGLVPMHOMNSDLSYLANFSPELMTNSPENSINLNCSS LGYPERKLEFLVNTENSTKIDYVKKSSQNNVBLIVVSLISFSVPAASNVSLFC VLQLESKLEPLSLYNTIDAHKPPDDDLILMALVILGVWFLLTKRRKKQ PGSHCEKTKYRKESQTKERVRYHETERSDEACVNISKASDNSTQF"
 996..1897
 /gene="CD86"
 BASE COUNT 585 a 400 c 383 g 529 t
 ORIGIN
 Query Match 47.2%; Score 169.4; DB 4; Length 1897;
 Best Local Similarity 87.2%; Pred. No. 4.1e-35;
 Matches 198; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
 QY 1 ATCAAGTTTACCAGAACTTAAGAGATGATATTTTCACTAAACACTGGAATTCACACT 60
 DB 486 ATACAGGTATACCCAGAACTGAGAGATGATATTTTGTGTAACCAAGATTCACAGT 545
 QY 61 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGTAACAGTT 120
 DB 546 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGTAACAGTT 605
 QY 121 TCTATGAGCTTGCTTTTTCAGTCCCTGAAGACACCAATGTGAGCGCTCTTTGTGCGCTG 180
 DB 606 TCTATGAGCTTGCTCTCTGCTCCCTGGAAGCAAGATGAGCACTCTCTGTGCTCG 665
 QY 181 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCATATAGA 227
 DB 666 CAACCTGAGTCAAT---GAACCTTCCTCCCTACCTTATATATAGA 709
 RESULT 7
 LOCUS BTA291475 924 bp mRNA linear MAM 14-OCT-2000
 DEFINITION Bos taurus partial mRNA for CD86 antigen (CD86 gene).
 ACCESSION AJ291475
 VERSION AJ291475.1 GI:1080379
 KEYWORDS
 SOURCE
 ORGANISM
 cow.
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 924)
 AUTHORS Brooke,G.P., Howard,C.J. and Parsons,K.R.

AUTHORS Nishimura, Y.
TITLE Direct Submission
JOURNAL Submitted (31-Jul-1999) Yorihiro Nishimura, Faculty of Agriculture,
The University of Tokyo, Department of Veterinary Microbiology;
1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan
(E-mail: yorihiro@oc.n.e.jip, Tel: +81-3-5841-5396,
Fax: +81-3-5841-8184)

COMMENT Sequence updated (08-Jun-2000).
FEATURES Location/Qualifiers

source

1..1270
/organism="Felis catus"
/db_xref="taxon:9685"
/cell_type="peripheral blood mononuclear cell"
240..1238
/gene="CD86"
240..1238
/gene="CD86"
/codon_start=1
/product="B-lymphocyte activation antigen B7-2 (CD86)"
/protein_id="BAB11688.1"
/db_xref="GI:9796388"
/translation="MGICDSTMGSLHTLLVMAALLSGVSSMKSOAYFNKTELPCHFT
NSONISLDELIVFMODDKLYLEIFRGENPQNVHLKKGRTSPDKDNTLRHNV
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SIOGYPEKEMFQLENTENSTKYDVTMKKQNNVLEIVNSISLPSVPEAHNVSVF
CALKLELLEMLSLPENIDAPKDKDEQGHFLMAVLVMEVFVCGWVSKTLRK
KKQPSHECETIKRERESKQNERVPHVPERSDAOCYNILKTAAGDKSTTHF"

CDS

polysignal 378 a 281 c 260 g 351 t
BASE COUNT 1245..1250
ORIGIN

Query Match 63.3%; Score 227.2; DB 4; Length 1270;
Best Local Similarity 94.8%; Pred. No. 1.3e-50;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 60
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DB 723 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 782
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTG 120
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DB 783 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTG 842
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
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DB 843 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 902
QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCTCAAAAG 240
|||||
DB 903 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCTCAAAAG 962
QY 241 GAGAGAAA 248
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DB 963 GATTAAGA 970

RESULT 4 2830 bp mRNA linear MAM 03-OCT-2001
LOCUS AY007704
DEFINITION Felis catus CD86 (CD86) mRNA, complete cds.
ACCESSION AY007704
VERSION AY007704.1 GI:15418725

KEYWORDS
SOURCE
ORGANISM
cat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE
AUTHORS Yang, S., Sellins, K.S., Powell, T., Stoneman, E. and Sim, G.K.
TITLE Novel transcripts encoding secreted forms of feline CD80 and CD86
JOURNAL Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)
MEDLINE 21390213

PUBMED 11498243
REFERENCE 2 (bases 1 to 2830)
AUTHORS Yang, S.

TITLE Direct Submission
JOURNAL Submitted (06-Sep-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA

FEATURES Location/Qualifiers

source
1..2830
/organism="Felis catus"
/db_xref="taxon:9685"
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/gene="CD86"
179..1177
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/codon_start=1
/product="CD86"
/protein_id="FAC23342.1"
/db_xref="GI:15418726"
/translation="MGICDSTMGSLHTLLVMAALLSGVSSMKSOAYFNKTELPCHFT
NSONISLDELIVFMODDKLYLEIFRGENPQNVHLKKGRTSPDKDNTLRHNV
IKDKGYHCFTIHKRGLVPMHOMSDSLVANSFQPELTYSNTENSIGIINLCS
SIOGYPEKEMFQLENTENSTKYDVTMKKQNNVLEIVNSISLPSVPEAHNVSVF
CALKLELLEMLSLPENIDAPKDKDEQGHFLMAVLVMEVFVCGWVSKTLRK
KKQPSHECETIKRERESKQNERVPHVPERSDAOCYNILKTAAGDKSTTHF"

BASE COUNT 877 a 570 c 586 g 797 t
ORIGIN

Query Match 63.3%; Score 227.2; DB 4; Length 2830;
Best Local Similarity 94.8%; Pred. No. 1.2e-50;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGGAATTCAACT 60
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DB 662 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGGAATTCAACT 721
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTG 120
|||||
DB 722 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTG 781
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
|||||
DB 782 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 841
QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCTCAAAAG 240
|||||
DB 842 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCTCAAAAG 901
QY 241 GAGAGAAA 248
|||||
DB 902 GATTAAGA 909

RESULT 5 901 bp mRNA linear PRI 06-SEP-2001
LOCUS AF344836
DEFINITION Papio cynocephalus anubis CD86 protein precursor, mRNA, complete
ACCESSION AF344836
VERSION AF344836.1 GI:13649983

KEYWORDS
SOURCE
ORGANISM
olive baboon.
Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.

REFERENCE
AUTHORS Villinger, F., Bostlik, P., Mayne, A.E., King, C.L., Genain, C.P.,
Weiss, W.R. and Ansari, A.A.
TITLE Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules
JOURNAL Immunogenetics 53 (4), 315-328 (2001)
MEDLINE 21383618

source 1..1795
/organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_type="peripheral blood mononuclear cells"
1..1795
/gene="CD86"
1..6
/gene="CD86"
7..849
/gene="CD86"
/function="counter-receptor for CD28 and CD152 (CTLA4)"
/note="lacks transmembrane domain; alternatively spliced"
/codon_start=1
/product="truncated B7-2 protein"
/protein_id="AA17298.1"
/db_xref="GI:6572519"
/translation="MYLRCITMELNLLFVNTLLLYGASMSQAYFNKGTGELPCHFTN
SNTSLDELVFMQDDKLVLYELRKEKPNQVHRRKGRFSFDKMMTLRLHNOI
KDKGLYOCFVHHKPKGLVPMHOMNSDLSYLANFSOPELIVTSNPTENGSIINTCS
IOGYPREKEMFLYKTEKNSSTKYDVTMKSONNVTELYNYSISLSPVEASNSVIFC
VIOLESMTPLSLPYNIETNKVERKESQTERVRYHETERSDEACVNIKTASGDS
TTOF"
850..1795
3'UTR
BASE COUNT 592 a 366 c 347 g 490 t
ORIGIN

Query Match 75.5% Score 271; DB 4; Length 1795;
Best Local Similarity 86.6% Pred. No. 2.3e-62;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 ATACAGGTTACCCAGAACCTTAGAGATGATTTTCAGCTAAACACTGAGATTCACT 60
|||||
DB 487 ATACAGGTTTACCCAGAACCTTAGAGATGATTTTTCAGCTAAACACTGAGATTCACT 546
|||||
QY 61 ACTAGTATGATGATGTCATGATGAAGAAATCTCAAAATATATGACAGAACTGACACGTT 120
|||||
DB 547 ACTAGTATGATGATGTCATGATGAAGAAATCTCAAAATATATGACAGAACTGACACGTT 606
|||||
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
|||||
DB 607 TCTATCAGCTTGCCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 666
|||||
QY 181 AAACGAGACACATGAGATGCTGCTCCCTACCTTTCAATATAGAAACATCAAAAG 240
|||||
DB 667 CAACGTGATCAAT---GAGGCTTCCCTCCCTACCTTATATATAGAAACATCAAAAGT 723
|||||
QY 241 GAGAGAAAAGAGACAAACAGACCAAGAGATGACATCAACGATGACGATCT 300
|||||
DB 724 GAGAGAAAAGAGAGACCAAGAGATGACATGACGATGACGATGACGATCT 783
|||||
QY 301 GATGAAGCCCACTGATTAACATTTGAAGACAGCGCTGAGCGACAAAGATCTACACA 359
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DB 784 GATGAAGCCCACTGATTAACATTTGAAGACAGCGCTGAGCGACCAAGATCTACACA 842
|||||

RESULT 2
AF157827 1138 bp mRNA linear MAM 08-MAY-2000
LOCUS AF157827
DEFINITION Felis catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
ORGANISM
cat.
Felis catus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedata; Felidae; Felis.
REFERENCE
AUTHORS Choi, I.-S., Hash, S.M., Winslow, B.J. and Collis, E.W.
TITLE Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
PUBMED 10713336

REFERENCE 2 (bases 1 to 1138)
AUTHORS Choi, I.-S., Hash, S., Winslow, B.J. and Collis, E.W.
TITLE Direct submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 km. 222, College Station, TX 77843, USA
FEATURES
source 1..1138
/organism="Felis catus"
/db_xref="taxon:9685"
1..1138
/gene="CD86"
63..1052
/note="B7-2 antigen"
/gene="CD86"
/product="start=1
/codon_start=1
/product="CD86 antigen"
/protein_id="A4D42974.1"
/db_xref="GI:5381424"
/translation="MGICDSTMGLSHTLLVALLLSGVSSMSQAYFNKGTGELPCHFT
NSNTSLDELVFMQDDKLVLYELRKEKPNQVHRRKGRFSFDKMMTLRLHNOI
KDKGTYHCHETIHKRGLVPMHOMNSDLSYLANFSOPELIVTSNPTENGSIINTCS
SIQSTPREKEMFLYKTEKNSSTKYDVTMKSONNVTELYNYSISLSPVEASNSVIFC
CALKLETLLEMLSLPNIIDAPKDPKDEGHEFLWLAAYLVFVFCGAVSRKTKRK
KQPGPSHECEITIKRERKESKQNERVPYHVERSDACVNIKTASGDRNQ"

BASE COUNT 358 a 245 c 246 g 289 t
ORIGIN

Query Match 63.3% Score 227.2; DB 4; Length 1138;
Best Local Similarity 94.8% Pred. No. 1.3e-50;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTTACCCAGAACCTTAGAGATGATTTTCAGCTAAACACTGAGATTCACT 60
|||||
DB 546 ATACAGGTTTACCCAGAACCTTAGAGATGATTTTTCAGCTAAACACTGAGATTCACT 605
|||||
QY 61 ACTAGTATGATGATGTCATGATGAAGAAATCTCAAAATATATGACAGAACTGACACGTT 120
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DB 606 ACTAGTATGATGATGTCATGATGAAGAAATCTCAAAATATATGACAGAACTGACACGTT 665
|||||
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
|||||
DB 666 TCTATCAGCTTGCCCTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 725
|||||
QY 181 AAACGAGACACATGAGATGCTGCTCCCTACCTTTCAATATAGAAACATCAAAAG 240
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DB 726 AAACGAGACACATGAGATGCTGCTCCCTACCTTTCAATATAGATGACACACTAAG 785
|||||
QY 241 GAGAGAAA 248
|||||
DB 786 GATTAAGA 793
|||||

RESULT 3
AB030652 1270 bp mRNA linear MAM 01-MAR-2001
LOCUS AB030652
DEFINITION Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86),
complete cds.
ACCESSION AB030652
VERSION AB030652.1 GI:9796387
KEYWORDS B-lymphocyte activation antigen B7-2 (CD86).
SOURCE Felis catus peripheral blood mononuclear cell cDNA to mRNA.
ORGANISM
Felis catus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedata; Felidae; Felis.
REFERENCE
AUTHORS Nishimura, Y., Shimomura, M., Miyazawa, T., Sato, E., Nakamura, K.,
Izumiya, Y., Ikeda, Y., Mikami, T. and Takahashi, E.
TITLE Molecular cloning of the cDNAs encoding the feline B-lymphocyte
activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
interact with human CTLA-19
JOURNAL Eur. J. Immunogenet. 27 (5-6), 427-430 (2000)
MEDLINE 20485322
PUBMED 10713336

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 491.57 Seconds
(without alignments) 15282.914 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccaccagaacc.....ggcgacaaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenDbml:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sy:*
- 12: gb_un:*
- 13: gb_vi:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
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- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	271	75.5	1795	4	AF106827	AF106827
2	227.2	63.3	1138	4	AF157827	AF157827
3	227.2	63.3	1270	4	AB030652	AB030652
4	227.2	63.3	2830	4	AY007704	AY007704
5	182.6	50.9	901	4	AF344836	AF344836
6	169.4	47.2	1897	4	AF106826	AF106826
7	145.6	40.6	924	4	BT9291475	BT9291475
8	124.6	34.7	994	4	PIGCD86G	PIGCD86G
9	124.6	34.7	994	6	AX027016	AX027016
10	111.4	31.0	164161	6	AC068630	AC068630
11	110	30.6	306	6	AR112784	AR112784
12	110	30.6	738	6	AX002781	AX002781
13	110	30.6	738	6	AX149548	AX149548
14	110	30.6	751	6	AR147737	AR147737
15	110	30.6	751	6	AR159759	AR159759
16	110	30.6	751	6	AR160451	AR160451
17	110	30.6	972	6	AX027005	AX027005
18	110	30.6	1002	6	AR147736	AR147736
19	110	30.6	1002	6	AR159758	AR159758
20	110	30.6	1002	6	AR160450	AR160450
21	110	30.6	1044	9	AF344851	AF344851
22	110	30.6	1048	9	AF344857	AF344857
23	110	30.6	1062	9	AF344861	AF344861
24	110	30.6	1112	9	HUMB72A	HUMB72A
25	110	30.6	1120	6	AR030780	AR030780
26	110	30.6	1120	6	AR112747	AR112747
27	110	30.6	1120	6	AR146413	AR146413
28	110	30.6	1120	6	AX047043	AX047043
29	110	30.6	1161	6	AR146414	AR146414
30	110	30.6	1424	6	AX330924	AX330924
31	110	30.6	1424	6	AX332506	AX332506
32	110	30.6	1424	6	HSU04343	HSU04343
33	110	30.6	2205	6	AX188198	AX188198
34	109.8	30.6	737	9	HSB725	HSB725
35	106.8	29.7	1062	9	AF344840	AF344840
36	102	28.4	1156	4	RABCD86B	RABCD86B
37	85	23.7	133	4	AF222915	AF222915
38	78	21.7	210	6	AR146418	AR146418
39	77.2	21.5	418	10	MMB72608	MMB72608
40	77.2	21.5	930	6	AX027012	AX027012
41	77.2	21.5	984	10	AF065897	AF065897
42	77.2	21.5	984	10	AF065898	AF065898
43	77.2	21.5	984	10	AF065899	AF065899
44	77.2	21.5	984	10	AF065900	AF065900
45	77.2	21.5	1115	10	S70108	S70108

ALIGNMENTS

RESULT 1
AF106827 1795 bp mRNA linear MAM 14-DEC-1999
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1795)
Yang, S. and Sim, G. K.
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
Immunogenetics 50 (5-6), 349-353 (1999)
JOURNAL
MEDLINE
20093996
REFERENCE
2 (bases 1 to 1795)
Yang, S. and Sim, G. K.
Direct Submission
Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 148..1134
 US-08-702-525-24

Query Match 41.8%; Score 212.6; DB 4; Length 1161;
 Best Local Similarity 69.0%; Pred. No. 9e-57;
 Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY 1 ATACAGGTTACCCAGACCTAAGAGATGATTTTCACTTAACCTGAGATTCACCT 60
 DB 625 ATACAGGTTACCCAGACCTAAGAGATGATTTTCTGTAAGACCAAGATTCACCT 684
 QY 61 ACTAAGTATGATCTGATGAGAAATCTCAAAATATGTGACAGACTGTACACGTT 120
 DB 685 ATCGAGTATGATGATTTATGACAGAAATCTCAAGATATGTCACAGAACTGTACGCGTT 744
 QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTTTTGTGCC 177
 DB 745 TCCATACGCTTGCTTTTTCATTCCTGATGTTACGACAAATATGCAATCTTCTGTATT 804
 QY 178 CTGAAGCTGAGACACTGAGATGCTCTCTCCCTACCTTTCATATAGATGCACAACT 237
 DB 805 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACTTTTCTCTATAG--AGCTT 855
 QY 238 AAGATTAAGACCTGAGAACAGGCCACTTCTGATTTCCGCTGTACTTGTATGTTT 297
 DB 856 GAGAGACCTGAGCCTCCCGACAGACACTTCTTGATTTACACTTCTTCTTCAACAGTT 915
 QY 298 GTTGTCTTTTGTGGATGATGCTCTTAAACACTAAGGAAAGAGAGAGAGCGCT 357
 DB 916 ATATATGATGATGATGTTTCTGTCTAATCTATGAAATGAGAAAGAGAGGCGCT 975
 QY 358 GGGCCCTCTCATGATGTGAACATCAAAAGGAGAGAAAGAGAGCAACAGACCAAC 417
 DB 976 CGCAACTCTTATTAATGTGAACCAACAAATGAGAGGAGAGAGTGAACAGACCAAG 1035
 QY 418 GAAGAGTACCATACAGTACTGAGAGATGATGAAGCCAGTG--TATTAACATT 474
 DB 1036 AAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGT 1095
 QY 475 TTGAAGACGCTCAGCGGACAAAAGTACTACA 507
 DB 1096 TCGAAGACATCTTCATGCGACAAAAGTACTACA 1128

RESULT 15
 PCT-US95-02576-24

; Sequence 24, Application PC/TUS9502576

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Novel forms of T Cell Costimulatory Molecules

; TITLE OF INVENTION: and Uses Therefor

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; FILING DATE: PCT/US95/02576

; PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/205,697
 FILING DATE: 02-Mar-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BWT-120CPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1161 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 148..1134
 PCT-US95-02576-24

Query Match 41.8%; Score 212.6; DB 5; Length 1161;
 Best Local Similarity 69.0%; Pred. No. 9e-57;
 Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY 1 ATACAGGTTACCCAGACCTAAGAGATGATTTTCACTTAACCTGAGATTCACCT 60
 DB 625 ATACAGGTTACCCAGACCTAAGAGATGATTTTCTGTAAGACCAAGATTCACCT 684
 QY 61 ACTAAGTATGATCTGATGAGAAATCTCAAAATATGTGACAGACTGTACAACTT 120
 DB 685 ATCGAGTATGATGATTTATGACAGAAATCTCAAGATATGTCACAGAACTGTACGCGTT 744
 QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTTTTGTGCC 177
 DB 745 TCCATACGCTTGCTTTTTCATTCCTGATGTTACGACAAATATGCAATCTTCTGTATT 804
 QY 178 CTGAAGCTGAGACACTGAGATGCTCTCTCCCTACCTTTCATATAGATGCACAACT 237
 DB 805 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACTTTTCTCTATAG--AGCTT 855
 QY 238 AAGATTAAGACCTGAGAACAGGCCACTTCTGATTTCCGCTGTACTTGTATGTTT 297
 DB 856 GAGAGACCTGAGCCTCCCGACAGACACTTCTTGATTTACACTTCTTCTTCAACAGTT 915
 QY 298 GTTGTCTTTTGTGGATGATGCTCTTAAACACTAAGGAAAGAGAGAGCGCT 357
 DB 916 ATATATGATGATGATGTTTCTGTCTAATCTATGAAATGAGAAAGAGAGGCGCT 975
 QY 358 GGGCCCTCTCATGATGTGAACATCAAAAGGAGAGAGAGAGAGCAACAGACCAAC 417
 DB 976 CGCAACTCTTATTAATGTGAACCAACAAATGAGAGGAGAGAGTGAACAGACCAAG 1035
 QY 418 GAAGAGTACCATACAGTACTGAGAGATGATGAAGCCAGTG--TATTAACATT 474
 DB 1036 AAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGT 1095
 QY 475 TTGAAGACGCTCAGCGGACAAAAGTACTACA 507
 DB 1096 TCGAAGACATCTTCATGCGACAAAAGTACTACA 1128

Search completed: October 19, 2002, 23:36:10
 Job time : 30.6516 secs

RESULT 12
 PCT-US95-02576-22
 Sequence 22: Application PC/TUS9502576
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 TITLE OR INVENTION: and Uses Therefor
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 City: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/02576
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/205,697
 FILING DATE: 02-Mar-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BWT-120CPCPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1120 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 107..1093
 PCT-US95-02576-22

Query Match	Similarity	69.0%	Pred. No. 8.8e-57;	DB 5;	Length 1120;
Best Local	Conservative	0;	Mismatches 144;	Indels 15;	Gaps 4;
Matches 354;					
QY	1	ATACAGGTTACCCAGAACCTTAAGGAGATGATATTTTCAGCTAAACACTGGAATTCACCT	60		
DB	584	ATACACGGTTACCCAGAACCTTAAGGAGATGAGATGATTTTGTCTAAGAACCAATTCACCT	643		
QY	61	ACTAAGTATATACCTGCATGAAAGAAATCTCAAAATATATGACAGAAAGCTTCACAGCTT	120		
DB	644	ATCGAGTATATGATATTTATGTCAGGAATCTCAAGATATATGTCACAGAACTGTACGAGCTT	703		
QY	121	TCTATTCAGCTTGGCTTTTTCAGTCCCTCAAG---CACACAATGTGAGACGCTTTTGTGCC	177		
DB	704	TCCATTCAGCTTGGCTTTTCATTCCTCCCTGATGTACGACCAATATGACCATCTTCGTATTT	763		
QY	178	CTGAAACTGAGACACTGAGAGATGGCGCTCCCTACCTTCATATATGATATGCAACAACCT	237		
DB	764	CTTGAAACTGACA---AGACGGCGCTTTATATCTTACCTCTCTCTATAG-----AGCTT	814		
QY	238	AAGGATTAAGACCCCTGACAGAGCCACTTCCTCTGATTTGGCGCTGATCTTGATATGTTT	297		
DB	815	GAGAGCCCTCAGGCTCCCGACACCAATCTCTGATTTAAGCTGTATATGCTTCCACAAGCTT	874		


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Query Match          41.8%:  Score 212.6:  DB 2:  Length 1120;
Best Local Similarity 69.0%:  Pred. No. 8.8e-57;
Matches 354;  Conservative 0;  Mismatches 144;  Indels 15;  Gaps 4;

QY      1  ATACAGGTATCCCGAAGACCTAAGAGAGATGTATTTTTCAGCTAAACACGTGAGATTCACACT 60
Db      584  ATACAGCGTTTACCAGAAACCTAAGAAAGATGAGTGTTTTGTCTAAGAACCAAGATTCACACT 643
QY      61  ACTAAGTGTGATCTGTCATGAGAAATCTCAAAATTAATGTGCAGAACTGTACACGTT 120
Db      644  ATCGATGTGATGTGATTAATGAGAAATCTCAAGATTAATGTCCACAGAACTGTACACGTT 703
QY     121  TCTATCAGCTTGCCCTTTTTCAGTCCCTGAG--CACAACAATGAGGGTCTTTTGTGCC 177
Db      704  TCCATCAGCTGTGTCTGTTTCATTCCTCTGATGTACGACCAATATGACCATCTTCTGTATT 763
QY     178  CTGAACACTGAGACACTGAGATGCTGCTCTCCCTACCTTTCATATATGATGACACACCT 237
Db      764  CTGGAACCTGACA--AGACGGGGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
QY     238  AAGGATTAAGACCCCTGAACAAGGCCACTTCTCTGATTTGGGGCTGTACTGTATGTTT 297
Db      815  GAGGACCCCTGACGCTCCGCCAGACACCAATCTCCGATTAACAGCTGACTTCCACAGCTT 874
QY     298  GTGTATTTTGTGGGATGCTGCTCTTAAACACTAAGAAAGAAAGAACAGACGCT 357
Db      875  ATTAATGTGTGATGATGTTTCTGTCTTAATTCATGTGAAGATGGAAGAAAGAGAGCGCTT 934
QY     358  GGCCCTCTCATGTAATGTGAAACCATCAAAAAGGAGAGAAAGAGAGCAACAGACCAAC 417
Db      935  CGCAACTCTTAAATGTGGAACCAACACAATGAGAGGAAAGAGAGACAGACCAAG 994
QY     418  GAAGAGTACCATACCAAGTACCTGAGAGATCTGATGTAAGCCCACTG---TATTAACATT 474
Db      995  AAAAGAGAAAAATTCATATACCTGAAAGATCTGATGAAGCCACAGCCGTTTAAAGT 1054
QY     475  TTGAAGACAGCCTCAGGCGACAAAGTACTCA 507
Db     1055  TCGAAGACATCTTCATGCGACAAAGTATACA 1087

RESULT 7
US-08-479-744A-1
: Sequence 1, Application US/08479744A
: Patent No. 6084067
: GENERAL INFORMATION:
: APPLICANT: Freeman, Gordon J.
: APPLICANT: Nadler, Lee M.
: TITLE OF INVENTION: Gray, Gary S.
: TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/479,744A
: FILING DATE: June 7, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION NUMBER: 08/280,757
: FILING DATE: 26-JUL-1994
: APPLICATION NUMBER: 08/109,393

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; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-479-744A-1

Query Match      41.8%; Score 212.6; DB 3; Length 1120;
Best Local Similarity 69.0%; Pred. No. 8.8e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY   1 ATCAAGGTTACCCCAACTTAAGSAGATATTTTCAGCTAAACACTSGAATTCAACT 60
Db   584 ATRACCGGTATCCCAACAACCTAAGAAGATGAAGTGTTTGTCTAAGAACCAAGAAATCAACT 643
QY   61 ACTAGATGATGATCTGTCATGAAAGAAATCTCAAATAATGTGACAGCAACTGTACAAGTT 120
Db   644 ATGCAGATGATGATGATATATGACAGAAATCTCAAGATATATGTCACAGCAACTGTACGAGCTT 703
QY   121 TCTATCAGCTGCGCTTTTTCAGTCCCTGAAG---CACACANTGTGACGCTTTTGTGCC 177
Db   704 TCACATCAGCTTGCTGTTTTTCATTCCTCATGTGTACGACCAATATGACCACTTCTGTATT 763
QY   178 CTGAACCTGGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACACAACCT 237
Db   764 CTGGAACAGTACAC---AGACGGGCTTTTATCTTCACACTTCTCTATAG-----AGCTT 814
QY   238 AAGGATTAAGAACCCCTGTAACAAGGCCACTTCTCTGATTTGGCGCTGTACTTGAATGTT 297
Db   815 GAGGACCTCAGCTGCTCCGCCAGACCAACATCTCTTGATTAGCCTGTACTTCCACAGATT 874
QY   298 GTTGTTTTTTTGNNGATGGTGTGCTTTTAAACACCTAAGGAAAAGAGAAAGACAGCCT 357
Db   875 ATTATATATGTTGATGTTTCTTCTGTCTAATTTCTATGAAATGGAAGAAGAAAGCGGCT 934
QY   358 GGCCCCCTCTCATGATGTGAACAACATCAAAAGGAGAGAAAAAGAGACAAACAGACCAAC 417
Db   935 CGCAACTCTTTAATAATGTGGAACCAACCAATGAGAGAGGAGAGAGTGAACAGACCAAG 994
QY   418 GAAGAGCTACACATACACAGCTACCTAGAGAGATCTATGAAGCCCAAGT---TATTAACT 474
Db   995 AAAGAGAAAATTCATATACCTTAAGATCTGATGAAGCCAGCGCTTTTAAAAAGT 1054
QY   475 TTGAAGACAGCCTCAGGGCAGCAAAAAGTACTACA 507
Db   1055 TCGAAGACATCTTCATGGCAGCAAAAAGTATACA 1087

RESULT 8
US-08-280-757B-1
; Sequence 1, Application US/08280757B
; Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,641
FILING DATE: 8-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-641-33

Query Match 41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAAATTCACCT 60
484 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAAATTCACCT 543
61 ACTAGATGATGATGCTGATGAAAGATCTCAAAATATGATGACAGAACTGTACAACT 120
544 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
121 TCTATCAGCTGCTTTTTCAGTCCCTGAAG--CACAACTGTGACGCTTTTGTGCC 177
604 TCCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
178 CTGAAGCTGAGACATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
664 CTGAAACTGACA--AGACGGGCTTTTATCTTACCTTCTCTATAG-----AGCTT 714
238 AAGATAAAGACCTGGAACAAGGCCACTTCTGATTCGGCTGATCTTGTATGTT 297
715 GAGGACCTCAGCTCCCGACAGACACATTCCTGATTCAGCTGATTCACACTTCTG 774
298 GTTGTGTTTGTGGATGCTGCTTTAAACACTAAGGAAAGAAAGAAAGACGCT 357
775 ATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
358 GGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
835 CGCAACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
418 GAAAGATACCATACCAAGTACCTGAGATGATGATGATGATGATGATGATGATGAT 474
895 AAAAGAGAAAAAATCCATATACCTGGAAGATGATGATGATGATGATGATGATGAT 954
475 TTGAGACAGCTTCAGGCGACAAAAGTACTACA 507
955 TCGAAGACATCTTCATGCGACAAAAGTACTACA 987

US-09-039-762A-33
Sequence 33, Application US/09039762A
Patent No. 6255073
GENERAL INFORMATION:
APPLICANT: Cal, Zelig
APPLICANT: Sprent, Jonathan
APPLICANT: Brummark, Anders

APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6255073th Wacker Drive, 36th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-762A-33

Query Match 41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGATTCACCT 60
484 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGATTCACCT 543
61 ACTAGATGATGATGCTGATGAAAGATCTCAAAATATGATGACAGAACTGTACAACT 120
544 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
121 TCTATCAGCTGCTTTTTCAGTCCCTGAAG--CACAACTGTGACGCTTTTGTGCC 177
604 TCCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
178 CTGAAGCTGAGACATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
664 CTGAAACTGACA--AGACGGGCTTTTATCTTACCTTCTCTATAG-----AGCTT 714
238 AAGATAAAGACCTGGAACAAGGCCACTTCTGATTCGGCTGATCTTGTATGTT 297
715 GAGGACCTCAGCTCCCGACAGACACATTCCTGATTCAGCTGATTCACACTTCTCA 774
298 GTTGTGTTTGTGGATGCTGCTTTAAACACTAAGGAAAGAAAGAAAGACGCT 357
775 ATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
358 GGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
835 CGCAACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
418 GAAAGATACCATACCAAGTACCTGAGATGATGATGATGATGATGATGATGATGAT 474


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; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-039-982A-33

Query Match      41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

Db      460 ATACAGGTTACCCAGAACCTAAGAGATGATGTTTCTAAGAACCAAGATTCACT 519
QY      61 ACTAAGTATGATACGTGCTAGAGAAATCTCAAAATTAATGTACAGACACTGACAGCTT 120
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QY      121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAG--CACACAATGTAGCGTCTTTTGTGCC 177
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QY      475 TTGAAGACAGCTCAGGCGACCAAAAGTACTACA 507
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RESULT 2

US-09-039-982A-33

; Sequence 33, Application US/09039982A

; Patent No. 6225042

; GENERAL INFORMATION:

; APPLICANT: Cal, Zeling

; APPLICANT: Sprent, Jonathan

; APPLICANT: Brummark, Anders

; APPLICANT: Jackson, Michael

; APPLICANT: Peterson, Per A

; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CELL

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Olson & Hierl, Ltd.

; STREET: 20 No. 6225042th Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/039,982A

; FILING DATE: 16-MAR-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Olson, Arne M.

; REGISTRATION NUMBER: 30,203

; REFERENCE/DOCKET NUMBER: TSRI4710

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 580-1180

; TELEFAX: (312) 580-1189

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; +

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; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-039-982A-33

Query Match      41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

Db      484 ATACAGGTTACCCAGAACCTAAGAGATGATGTTTCTAAGAACCAAGATTCAACT 543
QY      61 ACTAAGTATGATACGTGCTAGAGAAATCTCAAAATTAATGTGACAGACTGTACAGCTT 120
Db      544 ATCGAGTATGATGCTATTATGGAAGAAATCTCAAGATTAATGACAGAACTGTACAGCTT 603
QY      121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAG--CACACAATGTAGCGTCTTTTGTGCC 177
Db      604 TCCATCAGCTTCTGTGTTTCATTCCCTGATGTACGAGAAATGACAACTCTCTGTATT 663
QY      178 CTGAAGACTGGAACACTGGAAGATGCTGCTCTCACTTTCATATATGAGTCACAACT 237
Db      664 CTGGAAGACTGACA--AGACGGCGCTTTATCTTCACTTCTCTATAG-----AGCTT 714
QY      238 AAGGATTAAGACCTGACACAGCCACTTCTCTGATTTGGCGGTCTCTTGTATTGTTT 297
Db      715 GAGGACCCCTCAGCTCCGCCAGACCAATCTCTGATTTACGCTGTACTTCCACAGCTT 774
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Db      775 ATTATATGTGTATGTTTCTGTCTAATCTATGAAATGGAAGAGAGAGAGAGAGCTT 834
QY      358 GGCCCTCTCATGAAATGGAAGCAATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGCTT 417
Db      835 CGCAACTCTTATTAATGTGGAACCAACAAATGAGAGAGAGAGAGAGAGAGAGAGAGCTT 894
QY      418 GAAAGATACCATACAGTACCTGAGAGATCTGATGAGAGAGAGAGAGAGAGAGAGAGCTT 474
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QY      475 TTGAAGACAGCTCAGGCGACCAAAAGTACTACA 507
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RESULT 3

US-09-039-641-33

; Sequence 33, Application US/09039641

; Patent No. 6251627

; GENERAL INFORMATION:

; APPLICANT: Cal, Zeling

; APPLICANT: Sprent, Jonathan

; APPLICANT: Brummark, Anders

; APPLICANT: Jackson, Michael

; APPLICANT: Peterson, Per A

; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Olson & Hierl, Ltd.

; STREET: 20 No. 6251627th Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 17.6516 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-30

Perfect score: 509

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	212.6	41.8	972	4	US-08-848-760B-11
2	212.6	41.8	1002	4	US-09-039-882A-33
3	212.6	41.8	1002	4	US-09-039-641-33
4	212.6	41.8	1002	4	US-09-039-762A-33
5	212.6	41.8	1120	2	US-08-456-104-1
6	212.6	41.8	1120	2	US-08-101-624-1
7	212.6	41.8	1120	3	US-08-479-744A-1
8	212.6	41.8	1120	3	US-08-280-757B-1
9	212.6	41.8	1120	4	US-08-205-697A-22
10	212.6	41.8	1120	4	US-08-702-525-22
11	212.6	41.8	1120	4	US-08-403-253A-3
12	212.6	41.8	1120	5	PCT-US95-02576-22
13	212.6	41.8	1161	4	US-08-205-697A-24
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19	110	21.6	306	3	US-08-280-757B-46
20	110	21.6	751	4	US-09-039-882A-34
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22	110	21.6	751	4	US-09-039-762A-34
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29	77.2	15.2	1151	5	PCT-US95-02576-20	Sequence 20, Appl
30	77.2	15.2	1163	3	US-08-479-744A-22	Sequence 22, Appl
31	77.2	15.2	1163	3	US-08-280-757B-22	Sequence 22, Appl
32	77.2	15.2	1261	4	US-08-205-697A-12	Sequence 12, Appl
33	77.2	15.2	1261	4	US-08-702-525-12	Sequence 12, Appl
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37	31.4	6.2	2935	1	US-08-246-583-1	Sequence 1, Appl1
38	31.2	6.1	740	4	US-09-342-681C-99	Sequence 99, Appl
39	31	6.1	12047	2	US-09-022-461-1	Sequence 1, Appl1
40	30	5.9	2351	4	US-09-276-531-3	Sequence 3, Appl1
41	30	5.9	4865	3	US-08-894-017-24	Sequence 24, Appl
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43	29.6	5.8	1813	5	PCT-US94-12883-3	Sequence 3, Appl1
44	29.6	5.8	3138	1	US-07-867-106-4	Sequence 4, Appl1
45	29.6	5.8	14753	4	US-09-821-736-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-848-760B-11
Sequence 11, Application US/08848760B
Patent No. 6248721
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanhik, Lloyd & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-848-760B-11
Query Match 41.8%; Score 212.6; DB 4; Length 972;
Best Local Similarity 69.0%; Pred. No. 8.3e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;
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Oy	61	ACTAGATGATCTACTGTCATGAAACAAATCTCAAAATTAATGTGACAGACACTGTCAACGTT	120
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Oy	241	GATTAAGA	248
Db	119	GAGAGAAA	112

Search completed: October 19, 2002, 23:33:32
Job time : 89.1499 secs

DR WPI: 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1, Page 101-102; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;
Query Match 72.7%; Score 369.8; DB 20; Length 1897;
Best Local Similarity 85.7%; Pred. No. 8.1e-102;
Matches 436; Conservative 0; Mismatches 67; Indels 6; Gaps 2;
QY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACACTGAAATTTCACT 60
Db 1412 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACACTGAAATTTCAAGT 1353
QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAGCTT 120
Db 1352 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAGCTT 1293
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QY 301 GTTTTGTGGAGTGTCTCTTAAACACTAGGAAAGAGAGAGAGAGAGAGAGAGAG 360
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Db 938 ACAGCTCAGGCGCAAAAGTACTACACA 910
RESULT 13
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ID AAA49661 standard; cDNA; 1050 BP.
XX
AC AAA49661;
XX
DT 25-SEP-2000 (first entry)
XX
DE Pig costimulatory molecule CD86 (B7-2) cDNA.
XX
KM Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
XX xerotransplantation; organ transplant; vaccine; ss.

OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 36..1013
FT /tag= a
XX
FN WO200037102-A2.
XX
XX 29-JUN-2000.
PD
PE 17-DEC-1999; 99WO-GB04200.
XX
XX 19-DEC-1998; 98GB-0027921.
PR 23-OCT-1999; 99GB-0025015.
XX
XX (MLML-) ML LAB PLC.
XX
PI Lechler RI, Rogers NJ, Dorrling A;
XX
XX WPI: 2000-442537/38.
DR P-PsDB; AAY95321.
XX
PT Novel methods for improving tolerance to a xenograft comprising
PT immunizing a mammal with a T-cell epitope and a B-cell epitope -
PS disclosure; Fig 3; 81pp; English.
XX
CC The present sequence is that of cDNA clone CD86(1), which encodes
CC pig co-stimulatory molecule CD86 (B7-2) (see AAY95321). The clone
CC was obtained by PCR amplification of pig cDNA using primers (see
CC AAA49662-63) based on a published pig B7-2 sequence. The invention
CC relates to a novel strategy to inhibit costimulation by porcine
CC cells of human T cells, with particular importance in the context
CC of xerotransplantation of porcine organs. Recipients are immunised
CC with hybrid synthetic peptides comprising a T cell epitope
CC conjugated to sequences of the porcine costimulatory molecules
CC CD80, CD86 or CD40. Peptides that induce antibodies specific for
CC regions of costimulatory molecules involved in binding to their
CC counter-receptors on human cells (CD28 and CD14) are capable of
CC blocking the delivery of costimulation. Once the antibody response
CC has been induced, the transplanted organ will recall this response
CC due to the expression of the costimulatory molecules, thereby
CC sustaining the response, and providing an endogenous mechanism of
CC costimulatory blockade. The method is useful for improving the
CC tolerance of a host to xenografts, particularly porcine pancreatic
CC islet cells.
XX
SQ Sequence 1050 BP; 305 A; 260 C; 227 G; 258 T; 0 other;
Query Match 52.8%; Score 268.8; DB 21; Length 1050;
Best Local Similarity 75.5%; Pred. No. 2.6e-71;
Matches 391; Conservative 0; Mismatches 112; Indels 15; Gaps 4;
QY 1 ATCAAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACACTGAGAAATTTCACT 60
Db 495 ACACAGGCTACCCAGACCCAGAGAGATGATTTTCAGCTAACACTGAGAAATTTCAACC 554
QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAGCTT 120
Db 555 ACTGACATGATGCTGACATGAAGAAATCTCAAAATATGTGACAGAACTGTACAGCTT 614
QY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACACATGTGAGCGTCTTTTGCCCTG 180
Db 615 TCAATCAGGCTGCTCTCTCCATCCCTCCGAGACAAATGTGAGCATGCTGTCTCTG 674
QY 181 AAACGTGAGACATGAGATGCTGCTCCCTACCTTTGATATGATGATGATGATGATG 237
Db 675 CACCTTGAGCGCAAGACACTGCTTTTCTCCCTTCTGTAATATGATGACAAAGCA 734
QY 238 AAGATTAAGACCTGAGAACGCCACTTCTGTGATGCGCGTACTGTAAATGTTT 297
Db 735 CCGTGCAACCCCGTCTCCAGACACACATCTGTGATGACAGTCTACTGTACAGTG 794

Db 387 TCTATCAGCTTGTCTCTTCTCAGTCCCTGAAGACGAATGTACGATCTTCTGTCTCCTG 328
Qy 181 AAACGTGAGACACTGAGATGCTGTCTCCCTACCTTTCATATATAGATGACACACCTAAG 240
Db 327 CAACCTTAGTCAT---GAAGCTTCCCTCCCTACCTTATATATATAGATGACACA---TACG 274
Qy 241 GATAAAGACCCCTGACACAAAGCCATTCCTGTGATTTGGCGCTGTCTTGAATGTTTGT 300
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Qy 361 CCCTCTCATGAAATGTGAACCATCAAAAGGAGAGAGAAAAGAGACAAACAGACCAAGAA 420
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Db 33 ACAGCTTCAGGCGACACAGTACTACACA 5

RESULT 11
AAZ27913
ID AAZ27913 standard; DNA; 1897 BP.
XX

AC AAZ27913;

DT 20-DEC-1999 (first entry)

XX Canine B7-2 protein encoding DNA.

DE B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;

XX allergic reaction; infectious disease; tumor development; canine;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Canis familiaris.

OS

PN WO947558-A2.

PD 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

PF 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX

PI Slim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

DR P-PSDB; AAY41076.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

PT treating, e.g. autoimmune and atopic diseases

XX Claim 1; Page 97-99; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)

CC encoding nucleic acid molecules from dogs and cats. The proteins can be

CC expressed by standard recombinant methodology. The nucleic acid molecules

CC and the encoded proteins can be used for preventing or treating diseases,

CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

CC development, graft rejection, inflammation, arthritic and atopic diseases

CC such as atopic dermatitis. They can be used in mammals such humans, dogs,

CC cats, cattle, sheep or pets. The products can also be used for detection,

XX Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;
SQ
Query Match 72.7%; Score 369.8; DB 20; Length 1897;
Best Local Similarity 85.7%; Pred. No. 8,1e-102;
Matches 436; Conservative 0; Mismatches 67; Indels 6; Gaps 2;

Qy 1 ATACAGGTTACCCAGACCACTAAGAGATGTATTTTCAGCTAAACATGAAATTCACCT 60
Db 486 ATACAGGTTACCCAGACCACTAAGAGATGTATTTTCAGCTAAACATGAAATTCACCT 545
Qy 61 ACTAAGTATGATGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 546 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
Qy 121 TCTATCAGCTTGTCTCTTCTCAGTCCCTGAAGACACATGATGAGCGCTTTGTGCTG 180
Db 606 TCTATCAGCTTGTCTCTTCTCAGTCCCTGAAGACACATGATGAGCGCTTTGTGCTG 665
Qy 181 AAACGTGAGACACTGAGATGCTGTCTCCCTACCTTTCATATATAGATGACACACCTA 240
Db 666 CAACCTTAGTCAT---GAAGCTTCCCTCCCTACCTTTCATATATAGATGACACA---TACG 719
Qy 241 GATAAAGACCCCTGAAACAAAGGCGCACTTCTGTGATTTGGCGCTGATGATGATGAT 300
Db 720 AAACCCACCCCTGATGAGAGACACATCTCTGATTTGCGGCTGTGATGATGATGAT 779
Qy 301 GTTTTGTGAGTGTGTCTCTTAAACACTAAGAAAAGAAAGAAAGAGAGAGCTGAGC 360
Db 780 ATTCTGTGTGGATGTGTCTTCTTACACTATAGAAAAGAAAGAAAGAGAGAGCTGAGC 839
Qy 361 CCCTCTCATGAAATGTGAACCATCAAAAGGAGAGAGAAAAGAGACAAACAGACCAAG 420
Db 840 CCCTCTCATGAAATGTGAACCAAAAGTGAGAGAAAAGAAAGAGAGAGACCAAGAA 899
Qy 421 AGAGTACCATACAGCTACCTGAGAGATGTGATGAAAGCCCATGTATTAACATTTTGA 480
Db 900 AGAGTACGCTACCATGAAACGGAAGATCTGATGAAGCCCATGTGTAAACATTTTGA 959
Qy 481 ACAGCCTCAGGCGACAAAAGTACTACACA 509
Db 960 ACAGCTTCAGGCGACACAGTACTACACA 988

RESULT 12
AAZ27914/C
ID AAZ27914 standard; DNA; 1897 BP.
XX

AC AAZ27914;

DT 20-DEC-1999 (first entry)

XX Canine B7-2 gene complementary DNA sequence.

DE B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; canine;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Canis familiaris.

OS

PN WO947558-A2.

PD 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

PF 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX

PI Slim G, Yang S, Sellins KS;

XX

Db	835	CCCTCATGAAATGTGAAACCAACAAAGTGGAGAGAAAGAAAGTGAAGACAGACCAAGAA	894
Oy	421	AGAGTACCATACCAGCTACCTGAGAGATCTGATGAAGCCAGTGTAAACATTTTGAAG	480
Db	895	AGAGTACGGTACCATCAATGAACCGAAGATCTGATGAAGCCAGTGTAAACATTTTGAAG	954
Oy	481	ACAGCCTCAGGCGACAAAGTACTACACA	509
Db	955	ACAGCTTCAGCGACCAACAGTACTACACA	983
RESULT 10			
ID	AAZ27916/C		
XX	AAZ27916	standard; DNA; 987 BP.	
XX	AAZ27916;		
AC			
XX	20-DEC-1999	(first entry)	
XX			
DE		Complementary strand of canine B7-2 coding sequence.	
XX			
XX			
XX			
KW	B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;		
KW	allergic reaction; infectious disease; tumor development; canine;		
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.		
OS	Canis familiaris.		
OS			
XX	WO9947558-A2.		
PN			
XX	23-SEP-1999.		
XX			
PF	19-MAR-1999;	99WO-US06187.	
XX			
PR	19-MAR-1998;	98US-0078765.	
PR	17-APR-1998;	98US-0062597.	
XX			
PA	(HESK-) HESKA CORP.		
XX			
XX	Sim G, Yang S, Sellins KS;		
PI			
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for		
XX	treating, e.g. autoimmune and atopic diseases		
XX			
PS	Claim 1; Page 103-104; 148pp; English.		
XX			
CC	The invention provides B7 and CTLA4 (T cell costimulatory proteins)		
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be		
CC	expressed by standard recombinant methodology. The nucleic acid molecules		
CC	and the encoded proteins can be used for preventing or treating diseases,		
CC	e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor		
CC	development, graft rejection, inflammation, arthritic and atopic diseases		
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,		
CC	cats, cattle, sheep or pets. The products can also be used for detection,		
CC	diagnosis and drug screening.		
XX			
XX			
SO	Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;		
Query Match 72.7%; Score 369.8; DB 20; Length 987;			
Best Local Similarity 85.7%; Pred. No. 6e-102;			
Matches 436; Conservative 0; Mismatches 67; Indels 6; Gaps 2.			
Oy	1	ATACAAAGGTATCCCAAGAACTAAGAGATGTATTTTTCAGCTAAACACTGAGAATTCAACT	60
Db	507	ATACAAAGGTATCCCAAGAACTAAGAGATGTATTTTTCAGCTAAACACTGAGAATTCAACT	448
Oy	61	ACTAGATATGATACGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGTT	120
Db	447	ACTAGATATGATACGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGTT	388
Oy	121	TCTATACCTTGCCCTTTTTCAGTCCCTGGAAGCACAATGTGAGCGCTCTTTTGTGCCCTG	180


```
Db 726 AAACGTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATAGATGACAACTAAG 785
OY 241 GATTAAGACCCCTGACCAAGGCGACTTCCCTGTGATGTGGGCTGTACTGTATATGTTGTT 300
Db 786 GATTAAGACCCCTGACCAAGGCGACTTCCCTGTGATGTGGGCTGTACTGTATATGTTGTT 845
OY 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAGAAAGAAAGACAGCCCTGGC 360
Db 846 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAGAAAGAAAGACAGCCCTGGC 905
OY 361 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAACGAA 420
Db 906 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAACGAA 965
OY 421 AGAGTACCATACACGACTGACGAGATCTGATGATGAGCCCACTGATTAATTTGAAG 480
Db 966 AGAGTACCATACACGACTGACGAGATCTGATGATGAGCCCACTGATTAATTTGAAG 1025
OY 481 ACAGCCTCAGCGACAAAGT 501
Db 1026 ACAGCCTCAGCGACAAAGT 1046

RESULT 8
AA234785
ID AA234785 standard; cDNA; 1080 BP.
AC AA234785;
XX
DT 15-FEB-2000 (first entry)
XX
DE Cat CD86 (B7-2) cDNA.
XX
KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
KM FIV; feline leukaemia virus; feline infectious peritonitis virus;
KM feline panleukopenia virus; feline calicivirus; feline reovirus-3;
KM feline rotavirus; feline coronavirus; feline syncytial virus;
KM feline sarcoma virus; feline herpesvirus; feline borina disease;
KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
KM parasite; autoimmune disease; transplant rejection; therapy; ss.
XX
OS Fells domesticus.
XX
FH Key Location/Qualifiers
FT CDS 63..1055
FT /*tag= a
XX
XX MO9957271-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09502.
XX
XX 01-MAY-1998; 98US-0071699.
XX
XX (TEXA ) TEXAS A & M SYSTEM.
XX
XX Collison EM, Hash SM, Choi I;
XX
XX WPI: 2000-052972/04.
XX
XX P-PSDB; AAY32278.
XX
XX Novel feline proteins used to produce feline vaccines which prevent
XX infectious disease or to promote growth in homologous or heterologous
XX species -
XX
XX Claim 6; Fig 3A; 186pp; English.
XX
XX This is the nucleotide sequence of cDNA encoding feline CD86
XX (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
XX peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
XX comprising nucleic acid encoding feline CD86 ligand or feline
XX soluble CD80 ligand is designated PSI-2#19-2/011298 (ATCC 209821).
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CC The coexpression of CD86 with the costimulatory molecules CD28 (see
CC AA32279) and a tumour antigen or an antigen from a pathogenic
CC organism has the ability to activate or enhance activation of
CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
CC the ability to regulate activation of T-lymphocytes. The invention
CC provides isolated nucleic acids encoding feline CD86 ligand,
CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
CC (CD152) receptor, as well as vectors comprising the nucleic acids,
CC and polypeptides encoded by the nucleic acids. It also provides
CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
CC further comprising immunogens derived from pathogens, especially
CC feline immunodeficiency virus (FIV), feline leukaemia virus,
CC feline infectious peritonitis virus, feline panleukopenia virus,
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
CC herpesvirus, feline borina disease virus, rabies virus, chlamydia,
CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
CC pathogen, or parasite (all claimed). Vaccines capable of
CC enhancing an immune response, and vaccines capable of suppressing
CC an immune response (suitable for treating an autoimmune disease
CC or tissue or organ transplant rejection) are claimed. The
CC nucleic acids may be used for gene therapy or antisense therapy
CC protocols.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
XX
Query Match 97.5%; Score 496.2; DB 21; Length 1080;
Best Local Similarity 99.4%; Pred. No. 2.9e-140;
Matches 498; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAACAACAGATTCACACT 60
Db 546 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAACAACAGATTCACACT 605
OY 61 ACTAGTGTATCTGTCATGTAAGAAATCTCAAAATATGTGACAGACCTGACAACT 120
Db 606 ACTAGTGTATCTGTCATGTAAGAAATCTCAAAATATGTGACAGACCTGACAACT 665
OY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAACACACATGTGAGCGCTTTTGTGCCCTG 180
Db 666 TCTATCAGCTTGCTTTTTCAGTCCCTGAAACACACATGTGAGCGCTTTTGTGCCCTG 725
OY 181 AAACGTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAG 240
Db 726 AAACGTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAG 785
OY 241 GATAAAGACCTGGAACAAGGCGCACTTCTGTGATTCGGGCTGTACTGTATGTTGTT 300
Db 786 GATAAAGACCTGGAACAAGGCGCACTTCTGTGATTCGGGCTGTACTGTATGTTGTT 845
OY 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAGAAAGAAAGACAGCCCTGGC 360
Db 846 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAGAAAGAAAGACAGCCCTGGC 905
OY 361 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAACGAA 420
Db 906 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAACGAA 965
OY 421 AGAGTACCATACACGACTGACGAGATCTGATGATGAGCCCACTGATTAATTTGAAG 480
Db 966 AGAGTACCATACACGACTGACGAGATCTGATGATGAGCCCACTGATTAATTTGAAG 1025
OY 481 ACAGCCTCAGCGACAAAGT 501
Db 1026 ACAGCCTCAGCGACAAAGT 1046

RESULT 9
AA227915
ID AA227915 standard; DNA; 987 BP.
XX
XX AA227915;
```

PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS:
XX
DR WPI; 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 121-123; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;

Query Match 100.0%; Score 509; DB 20; Length 2830;
Best Local Similarity 100.0%; Pred. No. 5.9e-144; Mismatches 0; Indels 0; Gaps 0;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTTAACCTGAGAAATTCACCT 60
DB 2169 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTTAACCTGAGAAATTCACCT 2110

QY 61 ACTAAGATGATGCTCTGCTCAATGAAAGAAATCTCAAAATTAATGTACAGACCTGACACGTT 120
DB 2109 ACTAAGATGATGCTCTGCTCAATGAAAGAAATCTCAAAATTAATGTACAGACCTGACACGTT 2050

QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGCGCTTTTGTGCCCTG 180
DB 2049 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGCGCTTTTGTGCCCTG 1990

QY 181 AAACCTGAGACACACTGAGATGCTGCTCTCCCTACCTTTCAATATGATGCACACCTAG 240
DB 1989 AAACCTGAGACACACTGAGATGCTGCTCTCCCTACCTTTCAATATGATGCACACCTAG 1930

QY 241 GATAAAGACCTGAGACACACTGCTCTGATTTGGCGTGTACTGTATGTTTGT 300
DB 1929 GATAAAGACCTGAGACACACTGCTCTGATTTGGCGTGTACTGTATGTTTGT 1870

QY 301 GTTTTGTGGGATGCTGCTCTTTAAACACTAAGGAAAGAGACAGACGCTGGC 360
DB 1869 GTTTTGTGGGATGCTGCTCTTTAAACACTAAGGAAAGAGACAGACGCTGGC 1810

QY 361 CCCTCATGATGATGAAACCATCAAAAGGAGAGAAAAAGAGACCAACAGCA 420
DB 1809 CCCTCATGATGATGAAACCATCAAAAGGAGAGAAAAAGAGACCAACAGCA 1730

QY 421 AGAGTACCATACACGCTACCTGAGAGATGTGAAGCCCACTGATTAACATTTGAAG 480
DB 1749 AGAGTACCATACACGCTACCTGAGAGATGTGAAGCCCACTGATTAACATTTGAAG 1690

QY 481 ACAGCTCAGGGGACAAAGTACTACACA 509
DB 1689 ACAGCTCAGGGGACAAAGTACTACACA 1661

RESULT 7
AAZ34838
ID AAZ34838 standard; cDNA; 1080 BP.
XX
XX AAZ34838;
XX

DT 28-FEB-2000 (first entry)
XX
DE Feline CD86 (B7-2) cDNA.
XX
XX CD86; B7-2; feline; cat; recombinant virus; vaccine;
KW Immunomodulator; tumour; cancer; therapy; ss.
XX
XX Fells domesticus.
XX
XX
FT Key Location/Qualifiers
FT CDS 63..1052
FT /tag= a

W0957295-A1.
PN
PD 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09504.
PF
XX 01-MAY-1998; 98US-0071711.
PR
XX (SCHE) SCHERING-PLOUGH LTD.
PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.
PI Winslow BJ, Cochran MD;
XX
XX
DR WPI: 2000-062155/05.
DR P-PSDB: AAY32285.
XX
XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines
XX
XX
PS Disclosure; Fig 3A; 230pp; English.

CC This is the nucleotide sequence of cDNA coding for feline CD86
CC (B7-2). The cDNA was isolated from feline peripheral blood
CC mononuclear cell cDNA by PCR. Manipulating the expression of CD28
CC or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC regulates T cell proliferation and cytokine release. The invention
CC relates to a recombinant virus that contains at least one foreign
CC nucleic acid, inserted into a nonessential genomic region, that
CC encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
CC immunogenic fragments, and is expressed when the recombinant virus
CC is introduced into a suitable host. The invention also provides:
CC a recombinant virus further comprising a foreign nucleic acid
CC encoding an immunogen derived from a feline pathogen; recombinant
CC viruses capable of enhancing an immune response to protect against
CC disease; recombinant viruses expressing antisense sequences;
CC capable of suppressing an immune response in a feline, e.g. for
CC treatment of autoimmune disease or transplant rejection; and
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used
CC to reduce or eliminate a tumour in cats.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

Query Match 97.5%; Score 496.2; DB 21; Length 1080;
Best Local Similarity 99.4%; Pred. No. 2.9e-140; Mismatches 3; Indels 0; Gaps 0;
Matches 498; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTTAACCTGAGAAATTCACCT 60
DB 546 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTTAACCTGAGAAATTCACCT 605

QY 61 ACTAAGATGATGCTCTGCTCAATGAAAGAAATCTCAAAATTAATGTACAGACCTGACACGTT 120
DB 606 ACTAAGATGATGCTCTGCTCAATGAAAGAAATCTCAAAATTAATGTACAGACCTGACACGTT 665

QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGCGCTTTTGTGCCCTG 180
DB 666 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTAGCGCTTTTGTGCCCTG 725

QY 181 AAACCTGAGACACACTGAGATGCTGCTCTCCCTACCTTTCAATATGATGCACCAACCTAG 240
DB 181 AAACCTGAGACACACTGAGATGCTGCTCTCCCTACCTTTCAATATGATGCACCAACCTAG 240

```
QY 61 ACTAATGATGATCTGTCATGAAAGAAATCTCAAAATATGTCAGACACTGTACAACGTT 120
DB 453 ACTAAGATGATGATCTGTCATGAAAGAAATCTCAAAATATGTCAGACACTGTACAACGTT 394
QY 121 TCTATCAGCTTGGCTTTTTCAGTCCCGGAAGACACAAATGTAGGCTTTTGTGCCCTG 180
DB 393 TCTATCAGCTTGGCTTTTTCAGTCCCGGAAGACACAAATGTAGGCTTTTGTGCCCTG 334
QY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATATATAGATGCACAACCTAAG 240
DB 333 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATATATAGATGCACAACCTAAG 274
QY 241 GATTAAGACCTCTGAACAGGCCACTTCTCTGTGATTGCGGCTGTACTTGTATGTTTGT 300
DB 273 GATTAAGACCTCTGAACAGGCCACTTCTCTGTGATTGCGGCTGTACTTGTATGTTTGT 214
QY 301 GTTTTGTGAGATGGTGTCTTTTAAACAATGAGAAAGAAAGAAAGACAGCTGGC 360
DB 213 GTTTTGTGAGATGGTGTCTTTTAAACAATGAGAAAGAAAGAAAGACAGCTGGC 154
QY 361 CCCTCTCATGATGTGAAACCATCAAAAGGAGAGAAAGAAAGACAAACAGCAAGAA 420
DB 153 CCCTCTCATGATGTGAAACCATCAAAAGGAGAGAAAGAAAGACAAACAGCAAGAA 94
QY 421 AGAGTACCATACACACTGATGAGATCTGATGAAGCCAGTGTATTAACTTTTGAAG 480
DB 93 AGAGTACCATACACACTGATGAGATCTGATGAAGCCAGTGTATTAACTTTTGAAG 34
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
DB 33 ACAGCCTCAGGCGACAAAGTACTACACA 5

RESULT 5
AAZ27929
ID AAZ27929 standard; DNA; 2830 BP.
XX
AC AAZ27929;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 protein encoding DNA.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
DR P-PsDB; AAV41079.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g., autoimmune and atopic diseases
XX
PS Claim 1; Page 116-119; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
```

```
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other:
Query Match 100.0%; Score 509; DB 20; Length 2830;
Best Local Similarity 100.0%; Pred. No. 5,9e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTTCAGCTTAACACTGAGAAATTCACCT 60
DB 662 ATACAGGTTACCCAGAACCTAAGAGATGATTTTTCAGCTTAACACTGAGAAATTCACCT 721
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAACTGTACAACGTT 120
DB 722 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAACTGTACAACGTT 781
QY 121 TCTATCAGCTTGGCTTTTTCAGTCCCGGAAGACACAAATGTAGGCTTTTGTGCCCTG 180
DB 782 TCTATCAGCTTGGCTTTTTCAGTCCCGGAAGACACAAATGTAGGCTTTTGTGCCCTG 841
QY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATATATAGATGCACAACCTAAG 240
DB 842 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATATATAGATGCACAACCTAAG 901
QY 241 GATTAAGACCTCTGAACAGGCCACTTCTCTGTGATTGCGGCTGTACTTGTATGTTTGT 300
DB 902 GATTAAGACCTCTGAACAGGCCACTTCTCTGTGATTGCGGCTGTACTTGTATGTTTGT 961
QY 301 GTTTTGTGAGATGGTGTCTTTTAAACAATGAGAAAGAAAGAAAGACAGCTGGC 360
DB 962 GTTTTGTGAGATGGTGTCTTTTAAACAATGAGAAAGAAAGAAAGACAGCTGGC 1021
QY 361 CCCTCTCATGATGTGAAACCATCAAAAGGAGAGAAAGAAAGACAAACAGCAAGAA 420
DB 1022 CCCTCTCATGATGTGAAACCATCAAAAGGAGAGAAAGAAAGACAAACAGCAAGAA 1081
QY 421 AGAGTACCATACACACTGATGAGATCTGATGAAGCCAGTGTATTAACTTTTGAAG 480
DB 1082 AGAGTACCATACACACTGATGAGATCTGATGAAGCCAGTGTATTAACTTTTGAAG 1141
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
DB 1142 ACAGCCTCAGGCGACAAAGTACTACACA 1170

RESULT 6
AAZ27930/c
ID AAZ27930 standard; DNA; 2830 BP.
XX
AC AAZ27930;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 gene complementary DNA sequence.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
```

```
RESULT 3
AA227931
ID AA227931 standard; DNA: 996 BP.
XX
AC AA227931;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 protein coding sequence.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
DR P-PSDB; AAY41079.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 123-124; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;
Query Match 100.0%; Score 509; DB 20; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATACAGGTTACCCAGACCTTAAGAGATGTAATTTTCGCTAAACACTGAGAATTCACACT 60
DB 484 ATACAGGTTACCCAGACCTTAAGAGATGTAATTTTCGCTAAACACTGAGAATTCACACT 543
OY 61 ACTAGTGTGATGTCATGTAAGAAATCTCAAAATATGTAAGAGACTGTACACGTT 120
DB 544 ACTAGTGTGATGTCATGTAAGAAATCTCAAAATATGTAAGAGACTGTACACGTT 603
OY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
DB 604 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 663
OY 181 AAATGAGACACTGAGATGCTGCTCCCTACCTTTCAATATATGATGACACACTTAAG 240
DB 664 AAATGAGACACTGAGATGCTGCTCCCTACCTTTCAATATATGATGACACACTTAAG 723
OY 241 GATTAAGACCCGAGACAGGCGCACTTCGATGGATTTGGGCGTACTGTAATGTTTGT 300
DB 724 GATTAAGACCCGAGACAGGCGCACTTCGATGGATTTGGGCGTACTGTAATGTTTGT 783
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OY 301 GTTTTGTGGATGCTGTCCTTTAAACACTAAGGAAAGAGAGAGCAGCCTGGC 360
DB 784 GTTTTGTGGATGCTGTCCTTTAAACACTAAGGAAAGAGAGAGCAGCCTGGC 843
OY 361 CCCTTCATGATGTGTAACCATCAAAAGGAGAGAAAAAGAGCAAAACAGCAACGAA 420
DB 844 CCCTTCATGAAATGTGAAACATCAAAAGGAGAGAAAAAGAGCAAAACAGCAACGAA 903
OY 421 AGAGTCCATACACGCTACCTGAGAGATCTGATGAAAGCCAGTGTATTAACATTTTGAAG 480
DB 904 AGAGTCCATACACGCTACCTGAGAGATCTGATGAAAGCCAGTGTATTAACATTTTGAAG 963
OY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
DB 964 ACAGCCTCAGGCGACAAAGTACTACACA 992
RESULT 4
AA27932/C
ID AA27932 standard; DNA: 996 BP.
XX
AC AA27932;
XX
DT 20-DEC-1999 (first entry)
XX
DE Complementary strand of feline B7-2 coding sequence.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 124-125; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;
Query Match 100.0%; Score 509; DB 20; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 513 ATACAGGTTACCCAGACCTTAAGAGATGTAATTTTCAGCTAAACACTGAGAATTCACACT 454
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PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 PS Claim 1; Page 125-126; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.

XX Sequence 509 BP; 170 A; 109 C; 106 G; 124 T; 0 other;

Query Match 100.0%; Score 509; DB 20; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2.7e-144;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATACAAGGTTACCCAGACCTAAGAGAGATATTTTCAGTAACACTGAGATTCACACT 60
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 DB 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT 120
 OY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACACATGAGCGTCTTTTGCCCTG 180
 DB 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACACATGAGCGTCTTTTGCCCTG 180
 OY 181 AAACCTGGAGACACTGAGAGATGCTGCTCCCTACCTTCATATAGATGACACCTAAG 240
 DB 181 AAACCTGGAGACACTGAGAGATGCTGCTCCCTACCTTCATATAGATGACACCTAAG 240
 OY 241 GATAAAGCCCTGGAACAGGCGCCTCTCTGATTCGGGCTGTACTGTAAATGTTGTT 300
 DB 241 GATAAAGCCCTGGAACAGGCGCCTCTCTGATTCGGGCTGTACTGTAAATGTTGTT 300
 OY 301 GTTTTGTGGAGATGCTGCTCTTTAAACACTAAGGAAAGAAAGAACACGCTGGC 360
 DB 301 GTTTTGTGGAGATGCTGCTCTTTAAACACTAAGGAAAGAAAGAACACGCTGGC 360
 OY 361 CCTCTCATGATGTGAAGACCATCAAAAGGAGAGAAAGAGACCAACGAA 420
 DB 361 CCTCTCATGATGTGAAGACCATCAAAAGGAGAGAAAGAGACCAACGAA 420
 OY 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGTATTTAAG 480
 DB 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGTATTTAAG 480
 OY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
 DB 481 ACAGCCTCAGGCGACAAAGTACTACACA 509

RESULT 2
 AA27934/c
 ID AA27934 standard; DNA; 509 BP.

AA27934;

20-DEC-1999 (first entry)

XX Feline B7-2 gene (larger fragment) complementary DNA sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; feline;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 XX Felis catus;

XX WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-0506187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPL; 1999-571822/48.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 PS Claim 1; Page 127; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.

XX Sequence 509 BP; 124 A; 106 C; 109 G; 170 T; 0 other;

Query Match 100.0%; Score 509; DB 20; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2.7e-144;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATACAAGGTTACCCAGACCTAAGAGAGATATTTTCAGTAACACTGAGATTCACACT 60
 DB 509 ATACAAGGTTACCCAGACCTAAGAGAGATATTTTCAGTAACACTGAGATTCACACT 60
 OY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT 120
 DB 449 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT 390
 OY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACACATGAGCGTCTTTTGCCCTG 180
 DB 389 TCTATCAGCTGCTTTTTCAGTCCCTGAGACACACATGAGCGTCTTTTGCCCTG 330
 OY 181 AAACCTGGAGACACTGAGAGATGCTGCTCCCTACCTTCATATAGATGACACCTAAG 240
 DB 329 AAACCTGGAGACACTGAGAGATGCTGCTCCCTACCTTCATATAGATGACACCTAAG 270
 OY 241 GATAAAGCCCTGGAACAGGCGCCTCTCTGATTCGGGCTGTACTGTAAATGTTGTT 300
 DB 269 GATAAAGCCCTGGAACAGGCGCCTCTCTGATTCGGGCTGTACTGTAAATGTTGTT 300
 OY 301 GTTTTGTGGAGATGCTGCTCTTTAAACACTAAGGAAAGAAAGAACACGCTGGC 360
 DB 209 GTTTTGTGGAGATGCTGCTCTTTAAACACTAAGGAAAGAAAGAACACGCTGGC 360
 OY 361 CCTCTCATGATGTGAAGACCATCAAAAGGAGAGAGAAAGAGACCAACGAA 420
 DB 149 CCTCTCATGATGTGAAGACCATCAAAAGGAGAGAGAAAGAGACCAACGAA 420
 OY 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGTATTTAAG 480
 DB 89 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGTATTTAAG 480
 OY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
 DB 29 ACAGCCTCAGGCGACAAAGTACTACACA 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 : Search time 76.9499 Seconds

(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-30

Perfect score: 509
Sequence: 1 atacaaggtaccagaacc.....ggcgacaaagtactacaca 509

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	100.0	509	20	AAZ27933
2	509	100.0	509	20	AAZ27934
3	509	100.0	996	20	AAZ27931
4	509	100.0	996	20	AAZ27932
5	509	100.0	2830	20	AAZ27929
6	509	100.0	2830	20	AAZ27930
7	496.2	97.5	1080	21	AAZ34838
8	496.2	97.5	1080	21	AAZ34785
9	369.8	72.7	987	20	AAZ27915

c	10	369.8	72.7	987	20	AAZ27916	
c	11	369.8	72.7	1897	20	AAZ27913	
c	12	369.8	72.7	1897	20	AAZ27914	
c	13	268.8	52.8	1050	21	AAA49661	
c	14	227.2	44.6	359	20	AAZ27935	
c	15	227.2	44.6	359	20	AAZ27936	
c	16	212.6	41.8	972	20	AAV83208	
c	17	212.6	41.8	972	24	AAV83208	
c	18	212.6	41.8	1120	16	AAO81351	
c	19	212.6	41.8	1120	18	AAV49181	
c	20	212.6	41.8	1120	20	AAV55784	
c	21	212.6	41.8	1120	21	AAV55784	
c	22	212.6	41.8	1424	21	AAV83221	
c	23	212.6	41.8	1424	16	AAO85873	
c	24	212.6	41.8	2205	22	AAH72616	
c	25	169.6	33.3	840	20	AAZ27923	
c	26	169.6	33.3	840	20	AAZ27924	
c	27	169.6	33.3	1795	20	AAZ27921	
c	28	169.6	33.3	1795	20	AAZ27922	
c	29	110	21.6	306	18	AAV49198	
c	30	110	21.6	306	21	AAV49198	
c	31	110	21.6	738	20	AAV80293	
c	32	110	21.6	738	22	AAV80293	
c	33	110	21.6	764	18	AAV62939	
c	34	110	21.6	831	19	AAV03230	
c	35	99	15.2	210	16	AAV01038	
c	36	77.2	15.2	1151	20	AAV55785	
c	37	77.2	15.2	1151	16	AAO81366	
c	38	77.2	15.2	1163	18	AAV49182	
c	39	77.2	15.2	1163	21	AAV49182	
c	40	77.2	15.2	1161	16	AAV01046	
c	41	66	13.0	942	19	AAV99926	
c	42	40	7.9	593	20	AAH68957	
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ALIGNMENTS

RESULT 1	
AAZ27933	
ID AAZ27933 standard; DNA; 509 BP.	
AC AAZ27933;	
XX	
DT 20-DEC-1999 (first entry)	
XX	
DE Feline B7-2 protein (larger fragment) encoding DNA.	
XX	
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
KW allergic reaction; infectious disease; tumor development; feline;	
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
XX	
OS Felis catus.	
XX	
PN WO947558-A2.	
XX	
PD 23-SEP-1999.	
XX	
PF 19-MAR-1999; 99WO-US06187.	
XX	
PR 19-MAR-1998; 98US-0078765.	
XX	
PR 17-APR-1998; 98US-0062597.	
XX	
PA (HESK-) HESKA CORP.	
XX	
PI Sim G, Yang S, Sellins KS;	
XX	
XX WPI; 1999-571822/48.	
DR P-PDB; AAY41080.	
XX	

Complementary str
Canine B7-2 protei
Canine B7-2 gene c
Pig costimulatory
Feline B7-2 protei
Feline B7-2 gene (B7-2 CDNA. Homo s
Human co-stimulat
Human B lymphocyte
Human B lymphocyte
Human B7-2 antigen
Human B7-2 antigen
Human B lymphocyte
Human B7-2 CDNA.
B70 type B antigen
Human cervical can
Canine B7-25 prote
Complementary str
Canine B7-25 prote
Canine B7-25 gene
Human B lymphocyte
Human B7-2 constan
Human B7-2 extrace
Nucleotide sequenc
Chimeric human/po
DNA encoding CD86
Human B7-2 exon 5.
Mouse B7-2 antigen
Murine B lymphocyt
Mouse B lymphocyt
Murine B lymphocyt
Murine B lymphocyt
Mouse B7-2 exons m
Kat CD86 coding se
Human cervical can
Borrelia burgdorfe
Human cervical can
Angiogenesis prote

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLNL10296 row: k column: 20
High quality sequence stop: 283.

FEATURES

source

1. .858

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4473739"

/clone_lib="NIH_MGC_90"

/tissue_type="adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT

500 a 155 c 144 g 59 t

ORIGIN

Query Match

Best Local Similarity 8.0%; Score 40.8; DB 10; Length 858;
Matches 75; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 378 AACCATCAAAAGGAGAGAAAGAGAGCAACGAAAGCTACCTACCGCT 437

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QY 438 ACCTGAGAGATCTGATGAGCCAGTGTATTAACATTTTGAAGACAGCTCGGCGACAA 497

Db 524 AGCGGAAAAACCCACGCAAAAAAGAGCAATAACAAAGACAAACACACCGGAGAA 583

QY 498 AAGTACTACACA 509

Db 584 AAGAAAAAGGCA 595

RESULT 15

AA973397/c

LOCUS AA973397 378 bp mRNA linear EST 17-JUN-1998

DEFINITION o044a04.s1 NCI_CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1569006 3',
similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGENCD86 PRECURSOR ; mRNA sequence.
AA973397
AA973397.1 GI:3148577

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 378)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 501 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES

source

Location/Qualifiers

1. .378

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1569006"

/clone_lib="NCI_CGAP_Lu5"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT773 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

113 a 65 c 90 g 110 t

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 40.4; DB 9; Length 378;
Matches 60; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 437 TACCTGAGAGATCTGATGAGCCCAAGTG--TATTACATTTTGAAGACGCTCAGCG 493

Db 375 TACCTGAAAGATCTGATGAGCCCAAGCGGTGTTTAAAGTCGAGACATCTTCATGCG 316

QY 494 ACAAAAGTACTACA 507

Db 315 ACAAAAGTACTACA 302

Search completed: October 20, 2002, 04:30:10

Job time : 617.635 secs

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QY	489	AGGCGACAAAACTACTACA	507
Db	328	ATGCGACAAAAAGTGAATACA	310
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LOCUS	BG296224/c		
DEFINITION	602394048t1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4506082 5', mRNA sequence.		
ACCESSION	BG296224		
VERSION	BG296224.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 503)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM10380 Row: 0 Column: 11 High quality sequence start: 2 High quality sequence stop: 465. Location/Qualifiers 1..503		
FEATURES			
source	/organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:4506082" /clone_1ib="NIH_MGC_94" /tissue_type="retina" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."		
BASE COUNT	130 a 130 g 148 t 128 c		
ORIGIN			
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Db	482	TTTTTGTTTTGTGTTTTTTTTTTTTTTTCTTACGCTTGTTCTCTTAATAAACAAAG	423
QY	335	GGAAGAAGAGAGAGAGAGCGCTGGCCCTCTCATGAATGTGAACCATCAAAAGGAGA	394
Db	422	GGAACAGGAAATTCATTGACACACGTCATCTTAAGCTCAAACTAAATAACAGAAACA	363
QY	395	GAAAGAAGAGCAACAGACCAACGAAGAAGTACCTACACGCTACTGAGAGATCTGATG	454
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QY	455	AAGC 458	
Db	302	CAAC 299	
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DEFINITION	AL513871 LTR1.NFL006.PL2 Homo sapiens cDNA clone CLOB40022A07 3 prime, mRNA sequence.				
ACCESSION	AL513871				
VERSION	AL513871.1	GI:12777365			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 1101)				
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	unpublished (2001)				
FEATURES	<p>Contact: Genoscope</p> <p>Genoscope - Centre National de Sequencage</p> <p>Bp 191 J1006 Evry cedex - France</p> <p>Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.</p> <p>Location/Qualifiers</p> <p>1..1101</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="CLOB40022A07"</p> <p>/clone_id="LTR1.NFL006.PL2"</p> <p>/tissue_type="Placenta"</p> <p>/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"</p>				
BASE COUNT	162 a	33 c	248 g	323 t	335 others
ORIGIN					
Query Match	8.1%;	Score 41;	DB 9;	Length 1101;	
Best Local Similarity	33.9%;	Pred. No. 13;			
Matches	56;	Conservative 44;	Mismatches 65;	Indels 0;	Gaps 0;
OY	267	CCTCGCATTCGGCGCTGACTTGTATGTGTTGTTGTTGGATGCTGCTTTAA	326		
Db	181	CCCCBKRRKKKKKKKKBCBCKBKRRKKKKKKKKKKKKKKKKKKCBCKKRAA	122		
OY	327	AACACTAAGGAAAAGAGAAGAACACACCGCGCCCTCTCATGATGGAACCATCAA	386		
Db	121	AAA	62		
OY	387	AAGGAGAGAAAAGAGAGCAACAGACCAAGCAAGAAAGTACCATA	431		
Db	61	AAA	17		
RESULT 14	858 bp	mRNA	linear	EST 13-FEB-2001	
LOCUS	602365378F01 NIH_MGC_90	Homo sapiens	CDNA clone IMAGE:4473739 5'		
DEFINITION	BCG52809				
ACCESSION	BCG52809				
VERSION	BCG52809.1	GI:12762625			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 858)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	unpublished (1999)				
CONTACT	Robert Strausberg, Ph.D.				

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5212648"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 227 a 166 c 156 g 204 t

Query Match 16.5%; Score 84; DB 10; Length 753;
Best Local Similarity 81.8%; Pred. No. 1e-09; 25; Indels 2; Gaps 2;
Matches 121; Conservative 0; Mismatches 25; Indels 2; Gaps 2;

QY 1 ATACAGCTTACCCAGACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
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DB 585 ATACAGCTTACCCAGACCTAAGAGATG-AGTGTTCCTAAGAACCAAGAAATTCACCT 643

QY 61 ACTAGTATGATCTGTC-ATGAAGAAATCTCAAAATATGTCACAGACTGTACACGT 119
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DB 644 ATCCAGTATGATGTTATTTATGACAGAAATCTCAAGATATGTCACAGACTGTACACGT 703

QY 120 TTCATACAGCTTGCCTTTTTCAGTCCCT 147
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DB 704 TTCATACAGCTTGTCTGTTTCATTCCT 731

RESULT 8
A1750143/c 480 bp mRNA linear EST 22-JUN-1999
LOCUS A1750143
DEFINITION at27h10.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2356387 3' similar to SW:CD86, HUMAN P42081 T LYMHOCYTE
ACTIVATION ANTIGEN CD86 PRECURSOR ;, mRNA sequence.
ACCESSION A1750143
VERSION A1750143.1 GI:5128407
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thelsting, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40bp from G100
High quality sequence stop: 367.
Location/Qualifiers
1. 480
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2356387"
/clone_lib="Barstead aorta HPLRB6"

/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/note="Organ: aorta; Vector: PT73D-Pac (Pharmacia) with a
modified polylinker. Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACGAAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[5' ATTCGATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified PT733 vector. Library constructed by Bob
Barstead."

BASE COUNT 123 a 93 c 107 g 157 t

Query Match 15.4%; Score 78.6; DB 9; Length 480;
Best Local Similarity 74.6%; Pred. No. 1.9e-08;
Matches 126; Conservative 0; Mismatches 39; Indels 4; Gaps 2;

QY 342 GAAGAAGACGACCTGGCCCTCATGATGTGAACCATCAAGGAGAGAAAGA 401
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DB 475 GAAGAAGACGCGGCTCGCACTATATAATGTG-GACCAACAAATGAGAGGGAAGA 417

QY 402 GAGCAACGACCAACGAAAGATACCATCCAGCTGAGAGATCGTGAAGCCCA 461
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DB 416 GAGTGAACAGACCAAGAAAAAATCATTTACTGTAAGATGTGATGAAGCCCA 357

QY 462 GTG--TATTACATTTTGAAGACAGCTCAGCGCAAAAGTACTACA 507
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DB 356 GCGTGTTTTAAAGTTGCAAGACATCTTCAGCAAAAGTATACA 308

RESULT 9
BF137460 1002 bp mRNA linear EST 24-OCT-2000
LOCUS BF137460
DEFINITION 601780644F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008635 5',
mRNA sequence.
ACCESSION BF137460
VERSION BF137460.1 GI:10976500
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bcrf-nci.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M9243 row: h column: 12
High quality sequence stop: 663.
Location/Qualifiers
1. 1002
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4008635"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model MMT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 606.635 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-30
Perfect score: 509
Sequence: 1 atacaaggtaccagacc.....ggcgcacaaagtactacaca 509

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_estbhum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	241.8	47.5	9	AA056905	EST224F P
2	121.4	23.9	496	AW516826	AM516826 xq04h01.x
3	109.8	21.6	347	BG001664	RC4-GN006
4	108.8	21.4	543	BF064222	BF064222 7357b02.x
5	102.2	20.1	570	AT093604	ou82b09.s
6	97.4	19.1	504	AA946810	ou43c01.s
7	84	16.5	753	BI906246	603063172
8	78.6	15.4	480	AT750143	al27h10.x
9	57.8	11.4	1002	BF137460	601780644
10	54.8	10.8	486	BI132458	AR031A11L
11	42.2	8.3	391	AT632116	ls85b01.x
12	41.6	8.2	503	BG296224	602394048
13	41	8.1	1101	AL513871	AL513871
14	40.8	8.0	858	BG252809	602365378
15	40.4	7.9	378	AA973397	cod4a04.s
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23	38.6	7.6	1101	12	CNS04529	AL030588 Tetradon
24	38	7.5	1101	12	CNS00D03	AL075325 Drosophill
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33	37.2	7.3	981	9	AL664130	AL664130
34	37.2	7.3	386	10	BE921986	EST425755
35	37	7.3	512	12	AQ342188	RPCL11-12
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37	37	7.3	1072	12	AG186990	Pan. trogl
38	36.8	7.2	288	9	AM655358	105984 MA
39	36.8	7.2	327	10	BI294883	UI-R-DK0-
40	36.8	7.2	357	9	BE120284	UI-R-CAO-
41	36.8	7.2	382	10	H35362	EST110191 R
42	36.8	7.2	430	10	BG669718	BG669718 DRNAID07
43	36.8	7.2	441	9	AW530155	AW530155 UI-R-C4-a
44	36.8	7.2	502	10	BF564120	BF564120 UI-R-C4-a
45	36.8	7.2	790	3	BI644890	OP2677 M1

ALIGNMENTS

RESULT 1
AA056905/c 512 bp mRNA linear EST 18-SEP-1996
DEFINITION EST224F Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)
LOCUS Sus scrofa cDNA clone SPL224 forward similar to U25259 CTIA4

ACCESSION AA056905
VERSION AA056905.1 GI:1549545

KEYWORDS
SOURCE
ORIGINISM

REFERENCE
AUTHORS Tuggle C.K., Wahls S. and Schmitz C.
TITLE 1 (bases 1 to 512)
JOURNAL Unpublished (1996)
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ktuggle@iastate.edu

PCR Primers
FORWARD: TGCGGAGGACTCTG
BACKWARD: GACCGGCGTACGCT
Insert Length: 950 Std Error: 50.00
Seq primer: TGCGGAGGACTCTG.
Location/Qualifiers

FEATURES

source

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/clone="SPL224"
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/note="Oligo (dT) primed"

BASE COUNT 125 a 106 c 114 g 163 t 4 others

Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

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Db 584 ATACAGGTTTACCAGACCTTAGAGATGATTTTACCTTAACACCTGAGAAATTCACCT 643
QY 61 ACTAAGTATGATACGTGCTGATGAAAGAAATCTCAAAATATGTCACAGACTGTACACGTT 120
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QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
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Db 704 TCCATCAGCTTGCTGCTTTTCATTTCCCTGATGTACAGAGAAATATGACCATCTTCTGTATT 763
QY 178 CTGAAGCTGAGACACTGAGATGCTCTCTCCCTACCTTTCAATATGATGACACACCT 237
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Db 764 CTGGAAGACTGACA--AGACGGCGGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
QY 238 AAGGATTAAGACCTGGAACACGGCCACTTCTGTGATTTGGCGCTGACTTGTATTGTTT 297
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Db 935 CGCAACTCTTAAATTAATGTCGAACCAACATGAGAGAGGAAAGAGTGAACAGACCAAG 994
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QY 475 TTGAAGACAGCCTCAGGCGACAAAAGTACTACA 507
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RESULT 15

AR112747

LOCUS AR112747 1120 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 1 from patent US 6130316.

AR112747

ACCESSION AR112747.1 GI:14092647

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 1120)

AUTHORS

Freeman,G.J., Madler,L.M., Gray,G.S. and Greenfield,E.

TITLE

Fusion proteins of novel CTUA4/CD28 ligands and uses therefore

JOURNAL

Patent: US 6130316-A 1 10-Oct-2000;

FEATURES

location/Qualifiers

1..1120

source

/organism="unknown"

BASE COUNT

354 a 237 c 230 g 299 t

ORIGIN

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Query Match 41.8%; Score 212.6; DB 6; Length 1120;
Best Local Similarity 69.0%; Pred. No. 5.5e-49;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;
QY 1 ATACAGGTTTACCAGACCTTAGAGATGATTTTACCTTAACACCTGAGAAATTCACCT 60
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Db 584 ATACAGGTTTACCAGACCTTAGAGATGATTTTACCTTAACACCTGAGAAATTCACCT 643
QY 61 ACTAAGTATGATACGTGCTGATGAAAGAAATCTCAAAATATGTCACAGACTGTACACGTT 120
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Db 644 ATCGAGTATGATGATGATATGAGAAATCTCAAGATTAATCTACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
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Db 704 TCCATCAGCTTGCTGCTTTTCATTTCCCTGATGTACGAGCAATATGACCAATCTTCTGTATT 763
QY 178 CTGAAGCTGAGACACTGAGAGATGCTGCTCCTTACCTTTCAATATGATGACACACCT 237
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Db 764 CTGGAAGACTGACA--AGACGGCGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
QY 238 AAGGATTAAGACCTGGAACAGGCCACTTCTCTGATTTGGCGCTGACTTGTATTGTTT 297
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Db 815 GAGGACCCCTCAGCCTCCCGCCAGACACATCTCTGGAATTACAGCTGCTCCACACAGTT 874
QY 298 GTTGTGTTTTGTGGGATGCTGTCTCTTAAACACTAAGGAAAGAGAAAGAGACACCT 357
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Db 875 ATTATATGTGTATGATGTTTCTGTCTAATTTCTATGGAATATGGAAGAAAGAGCGCCT 934
QY 358 GGGCCCTCTCATGATGTCGTAACCATCAAAAGGAGAGAGAAAGAGACAAACAGCAAC 417
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 935 CGCAACTCTTAAATATGTCGAACCAACATGAGAGAGGAAAGAGTGAACAGACCAAG 994
QY 418 GAAAGATACCATACAGCTACCTGAGAGATCTGATGAAGAGCCAGTG--TATTACATT 474
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Db 995 AAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCCGAGCGTGTTTTAAAGT 1054
Db 1055 TCGAAGACATCTTCATGCGACAAAAGTGATACA 1087

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Search completed: October 20, 2002, 03:16:48
 Job time : 723.962 secs

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QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGACAGAACTGACAGCTT 120

Db 544 ATCGAGTATGATGATGATGAGAAATCTCAAGATATGACAGAACTGACAGCTT 603

QY 121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAG---CACACAAATGAGGCTTTTGTGCC 177

Db 604 TCCATCAGCTTCTGTTTTCATCTCCCTATGATGACAGAAATGACCAATCTCTGTATT 663

QY 178 CTGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATATGATGACAACT 237

Db 664 CTGGAAGTGTGAC---AGACGCGGCTTTTATCTTCATCTCTCTATGAG-----AGCTT 714

QY 238 AAGGATTAAGACCTTGACAAAGGCTTCTCTGATGTTGGGCTGTCTGTATGTTT 297

Db 715 GAGGACCTCTCAGCTCCCTCCAGACCAATCTCTGATTAAGCTGATCTTCAACACTT 774

QY 238 GTTGTTTTTTGTGGATGCTGCTCTTAAACACTAAGAAAGGAGAAAGACAGCTT 357

Db 775 ATTATATGATGATGATGTTTCTGCTATCTATGAGAAATGAGAAAGAGGAGCTT 834

QY 358 GGGCCCTCTCATGATGATGAAACCAATCAAAAGGAGAGAAAGACAGCAACACCAAC 417

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QY 418 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474

Db 895 AAGAGAGAAAGAAATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 954

QY 475 TTGAAGACAGCTCTCAGGCGCAAAAGTACTACA 507

Db 955 TCGAAGACATCTTTCATGCGACAAAGTGTATCA 987

RESULT 13

HOMB72A

LOCUS HOMB72A 1112 bp mRNA linear PRI 31-DEC-1994

DEFINITION Human CTIL4 counter-receptor (B7-2) mRNA, complete cds.

ACCESSION L25259

VERSION L25259.1 GI:416368

KEYWORDS CTIL4 counter-receptor.

SOURCE Homo sapiens cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1112)

AUTHORS Freeman,G.J., Gribben,J.G., Bousiotis,V.A., Ng,J.W., Restivo,V.A., Jr., Lombard,L.A., Gray,G.S. and Nadler,L.M.

TITLE Cloning of B7-2: a CTIL4 counter-receptor that costimulates human T cell proliferation [see comments]

JOURNAL Science 262 (5135), 909-911 (1993)

MEDLINE 94053735

FEATURES

source

1..1112 Location/Qualifiers

/organism="Homo sapiens"

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1..1112

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107..1096

/gene="B7-2"

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/translation="MDPQCTGLSNILFVNAFLISGAAPLKIQAVENETADLPQCPAN SONSLSELVFWQDENILVNEVLEGEKEDSVHSKXMGRTSDSWSLRLNLDOI KDGLYOCIIHKKPTGMIIRIHOHMSSELVANSOPEIIVISNTEVYINTCSSI HGYPEPKMSVILRTKNSITIDGIMKSDONVEIDVSIISVSPDVSNNITIC ILEFDKTRLLSPSIEIREDPOPBDHLPATLPIYIICVMWFCILMKKKRRP RNSYKCGTINIERESEOTKKREKIHIPERSEDAORVFKSKTSKCDKSDICP"

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mat_peptide /gene="B7-2" 176..1093

polya_site /product="CTIL4 counter-receptor" 1112

BASE COUNT 346 a 237 g 230 g 299 t

ORIGIN

Query Match 41.8%; Score 212.6; DB 9; Length 1112;

Best Local Similarity 69.0%; Pred. No. 5.5e-49;

Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

1 ATCAAGGTTACCCAGAACTAGAGATGATGTTTTGCTAAGACCAAGATTCAACT 60

Db 584 ATACAGGTTATCCAGAACCTAAGAGATGATGTTTTGCTAAGAACCAAGATTCAACT 643

QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGACAGAACTGACAGCTT 120

Db 644 ATGAGTATGATGATGATGATGAGAAATCTCAAGATATGACAGAACTGACAGCTT 703

QY 121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAG---CACACAAATGAGGCTTTTGTGCC 177

Db 704 TCCATCAGCTTCTGTTTTCATCTCCCTGATGATGATGATGATGATGATGATGAT 763

QY 178 CTGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATATGATGACAACT 237

Db 764 CTGAAGTGTGAC---AGACGCGGCTTTTATCTTCACTTCTCTATGAG-----AGCTT 814

QY 238 AAGGATTAAGACCTTGACAAAGGCTTCTCTGATGTTGGGCTGTCTGTATGTTT 297

Db 815 GAGGACCTCTCAGCTCCCTCCAGACCAATCTCTGATTAACAGCTGTACTTCCACAGTT 874

QY 298 GTTGTTTTTTGTGGATGCTGCTCTTAAACACTAAGAAAGGAGAAAGACAGCTT 357

Db 875 ATTATATGATGATGATGTTTCTGCTATCTTCTATGAAATGAGAAAGAGAGCGGCTT 934

QY 358 GGGCCCTCTCATGATGATGAAACCAATCAAAAGGAGAGAAAGACAGCAACACCAAC 417

Db 935 CGCACTCTTATTAATGATGAGAAACCAATGAGAGGAGAGATGAGTGAACAGCAAG 994

QY 418 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474

Db 995 AAGAGAGAAAGAAATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1054

QY 475 TTGAAGACAGCTCTCAGGCGCAAAAGTACTACA 507

Db 1055 TCGAAGACATCTTTCATGCGACAAAGTGTATCA 1087

RESULT 14

AR030780

LOCUS AR030780 1120 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5861310.

ACCESSION AR030780

VERSION AR030780.1 GI:5943994

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1120)

AUTHORS Freeman,G.J., Nadler,L.M. and Gray,G.S.

TITLE Tumor cells modified to express B7-2 with increased immunogenicity and uses therefor

JOURNAL Patent: US 5861310-A 1 19-JAN-1999;

MEDLINE

FEATURES

source

1..1120 Location/Qualifiers

/organism="unknown"

BASE COUNT 354 a 237 c 230 g 299 t

ORIGIN

Query Match 41.8%; Score 212.6; DB 6; Length 1120;

Best Local Similarity 69.0%; Pred. No. 5.5e-49;

LOCUS	ARI47736	1002 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	Sequence 33 from patent US 6225042.				
ACCESSION	ARI47736				
VERSION	ARI47736.1	GI:15111826			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1002)				
TITLE	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.				
JOURNAL	Antigen presenting system and methods for activation of T-cells				
FEATURES	Patent: US 6225042-A 33 01-MAY-2001;				
source	Location/Qualifiers				
	1..1002				
BASE COUNT	/organism="unknown"				
ORIGIN	309 a 215 c 203 g 275 t				
Query Match	41.8%; Score 212.6; DB 6; Length 1002;				
Best Local Similarity	69.0%; Pred.No.5.5e-49;				
Matches	354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;				
QY	1 AATCAAGCTTACCCAGAACCTAAGAGATGTATTTCACGTAACACGTGAGATTCAACT	60			
DB	484 AATCAAGCTTACCCAGAACCTAAGAGATGTATTTCACGTAACACCAAGAACTCAACT	543			
QY	61 ACTAAGTATGATACGTCTGTGAAGAAATCTCAAAATTAATGTACACGAACCTGACACGTT	120			
DB	544 ATCGATATGATGATATTATATGACAAATCTCAAGTAATATGTACAGAACTGACACGTT	603			
QY	121 TCTATACGCTTCCTCTTTTTCAGTCCCTGAG--CACACATGTGAGCGCTCTTTTGTGCC	177			
DB	604 TCCATTCAGCTGTCTGTTTCATTTCCCTGATGTTTACGAGCAATATGACCATCTTCTGTATT	663			
QY	178 CTGAACATGAGACACTGGAGATGCTGCTCTCCCTACCTTTCATATATGATGACACACCT	237			
DB	664 CTGGAAGACTGACA---AGACGGCGCTTTTATCTTACCTTTCTCTATAG-----AGCTT	714			
QY	238 AAGGATTAAGACCTGGAACAAGCGCATCTCTCTGATGTGGCTGTACTTGTAAATGTTT	297			
DB	715 GAGGACCTCTGACCTCCGCCACAGACCAACATTCCTTGATTAACGCTGTACTTCCACAGTT	774			
QY	298 GTTGTTTTTTGTGGATGSGTGTCTTAAACACATCAAGGAAAGGAAGAAGAGAGCTT	357			
DB	775 ATTATATGTGTGATGTCTTTTCTGTCTAATTTCTATGGAATGGAAGAAAGAGCGGCTT	834			
QY	358 GGCCCTCTCATGATGTGAACCATCTCAAAAGGAGAGAAAGAGAGCAACAGACCAAC	417			
DB	835 CGCACTCTTATTAATATGTGAACCAACAACTATGAGAGGAAAGAGATGAGAACGACCAAG	894			
QY	418 GAAAGATGATCACTTACCACGTACTAGAGATCTGTATGAAGCCCACTG--TATTACATT	474			
DB	895 AAAAAGAAAAAATCCATATACCTGAAGAAGATCTGTATGAAGCCCACTGTTTAAAAAGT	954			
QY	475 TTGAAGACAGCCTCAGCGACAAAAGTACTACA	507			
DB	955 TCGAAGACATCTTCAATGCGACAAAAGTATACA	987			
RESULT 11					
LOCUS	ARI159758	1002 bp	DNA	linear	PAT 17-OCT-2001
DEFINITION	Sequence 33 from patent US 6251627.				
ACCESSION	ARI159758				
VERSION	ARI159758.1	GI:16222530			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1002)				
TITLE	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.				
JOURNAL	Antigen presenting system and methods for activation of T-cells				
PATENT	Patent: US 6251627-A 33 26-JUN-2001.				

FEATURES	source	location/Qualifiers
		1..1002 /organism="unknown"
BASE COUNT	309 a 215 c 203 g 275 t	
ORIGIN		
Query Match	41.8%;	Score 212.6; DB 6; Length 1002;
Best Local Similarity	69.0%;	Pred. No. 5.5e-49;
Matches 354;	Conservative 0;	Mismatches 144; Indels 15; Gaps 4
QY	1	ATACAAAGTTACCCAGAACCTTAAGAGATGTAATTTTCACCTAAACCTGAGATTCAACT 60
DB	484	ATACACGGTTACCCAGAACCTTAAGAGATGAGTGTCTTCTTAAGAACCAAGATTCAACT 543
QY	61	ACTAAGTATGATACAGTGCATGTAAGAAATGCAAAATATGTCAGACACTGTAACAGCTT 120
DB	544	ATCGAATATGATAGTATTTATGCAAGAAATCTCAAGATTAATGTCACGACACTGTACGACGTT 603
QY	121	TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG--CACACAAATGTGAGCGCTTTTGTGCC 177
DB	604	TCCATCAGCTTGTCTGTTCATTCCTCGATGTATGACGACAAATATGACATCTCTGTATT 663
QY	178	CTGAACACTGGAACACTGSAAGATGCTGCTCTCCCTACCTTCAATTAATGACACAACT 237
DB	664	CTGGAAGACTGACA--AGACGGGCGCTTTATCTTCACTTCTATAG----AGCTT 714
QY	238	AAGCAATAAAGACCTGCAACAGGCAAGGCACTCTCTGTGATTCGCGCTGTACTGTATATGTT 297
DB	715	GAGGACCCCTCAGCGCTCCCGACACCAATCTCTGTGATTAACAGCTGTACTTCCAAACAGTT 774
QY	298	GTTGTGTTTTTGTGGGATGSGTGTCTTTAAACACTTAAGAAAAAGAAAGAACGACGCT 357
DB	775	ATTATATGTGTGATGATGTTTTCTGTCTAAATTCATGTGAATGTGAAGAAAGAAAGCGCGCT 834
QY	358	GGCCCTCTCATGAATGTGAACCATCAAAAGGAGAGAGAAAGAGAGCAACGACCAAC 417
DB	835	CGCACTCTTATTAATGTGGAACCAACAAATGTGAGAGAGGAAAGAGAGTGAACGACCAAG 894
QY	418	GAAAGATACCAATACCAGCTACCTGAGAGATCTGATGAAGCCAGTG--TATTAACATT 474
DB	895	AAAAAGAGAAAAATCCATCTATACCTGAAGATCTGATGAAGCCAGCGTGTTTTAAAGT 954
QY	475	TTGAAGACAGCCTCAGGCGCAAAAGTACTACA 507
DB	955	TGGAAGACATCTTCAATGCGACAAAGTGTATCA 987
RESULT 12		
ARI60450		
LOCUS	ARI60450	1002 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 33 from patent US 6255073.	
ACCESSION	ARI60450	
VERSION	ARI60450.1	GI:16224366
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 1002)	
AUTHORS	Cal,Z., Sprent,T., Brunmark,A., Jackson,M. and Peterson,P.A.	
TITLE	Antigen presenting system and methods for activation of T-cells	
JOURNAL	Patent: US 6255073-A 33 03-JUL-2001;	
FEATURES	location/Qualifiers	
source	1..1002	
BASE COUNT	309 a 215 c 203 g 275 t	
ORIGIN		
Query Match	41.8%;	Score 212.6; DB 6; Length 1002;
Best Local Similarity	69.0%;	Pred. No. 5.5e-49;
Matches 354;	Conservative 0;	Mismatches 144; Indels 15; Gaps 4;
QY	1	ATACAAAGTTACCCAGAACCTTAAGAGATGTAATTTTCACGCTTAACACTGAGATTCAACT 60

ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Macaca.
AUTHORS	1 (bases 1 to 1048) Villinger, F., Postik, P., Mayne, A.E., King, C.L., Genain, C.P., Weiss, W.R. and Ansari, A.A.
TITLE	Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules
JOURNAL	Immunogenetics 53 (4), 315-328 (2001)
MEDLINE	21383618
PUBMED	11491535
REFERENCE	2 (bases 1 to 1048)
AUTHORS	Villinger, F.
TITLE	Direct Submission
JOURNAL	Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory University School of Medicine, Winship Cancer Institute, 1365B Clifton Rd, Atlanta, GA 30322, USA
FEATURES	Location/Qualifiers
source	1..1048
	/organism="Macaca mulatta"
	/db_xref="taxon:9544"
sig_peptide	19..68
CDS	19..990
	/note="B7.2"
	/codon_start=1
	/product="CD86 protein precursor"
	/protein_id="AAK37540.1"
	/db_xref="GI:13650012"
	/translation="MGLSNLLFVAFLLISGADPLIKIAYENETADLPQFANSONRSLS SELVEWQMENTVLNVEVYLKERFDSVHSKMYGRTSFDPESWTLRHNLQIKKGLY QCILHHRKRGMLRHHOMNSLSVLANSOPELVISNIENMYINTLCSIHYPBEK EKMSVLLRTKRTSTIEYGVOMQSODNTELDVSISSVSPDYTSMTTICVLETRK TOLLSPESTLEDPQPPDHPHPIWITVPLVILCVAFCLILKKMKKKQPRRSYKCK GTNMEERESQRTKKRKINVERPSDAQCFKSLKPKRSCKSTPR"
BASE COUNT	324 a 230 c 205 g 289 t
ORIGIN	
Query Match	42.3%; Score 215.2; DB 9; Length 1048;
Best Local Similarity	69.3%; Pred. No. 1e-49;
Matches 356; Conservative	0; Mismatches 143; Indels 15; Gaps 4;
QY	1 ATACAGGTTGCCGACGACCTTAAGAGATGTAATTTTCAGTCAACGACGATTCACCT 60
DB	478 ATACAGGTTGCCGACGACCTTAAGAGATGTAATTTTCAGTCAACGACGATTCACCT 537
QY	61 ACTAAGTATGATACGTATGATGAAGAATCTCAAAATTAATGTGACAGACTGTACACGTT 120
DB	538 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
QY	121 TCTATTCAGCTTGCTTTTTCAGTCCCTGAG--CACACATGTGACGCTCTTTTGTGCC 177
DB	598 TCCATCAGCTTGCTTGCTTTTCAGTCCCTGAG--CACACATGTGACGCTCTTTTGTGCC 657
QY	178 CTGAACAGTGACACTGGAGATGTGCGTCCTTACCTTCATATGATGATGACACACT 237
DB	658 CTGGAAGTACGACACTGGAGATGTGCGTCCTTACCTTCATATGATGATGACACACT 708
QY	238 AAGGATTAAGACCTTGACACAGGACGACCTTCTGTGATTTGGGCTGTACTTAAATGTTT 297
DB	709 GAGGACCTTGACACCTTGACACAGGACGACCTTCTGTGATTTGGGCTGTACTTAAATGTTT 768
QY	298 GTTGTGTTTGGGATGSGTGTCTTAAACACATGAAGAAAGAAAGAAAGAGAGAGCCT 357
DB	769 ATTATATGTGTGATGCTTTCTGTCTAATTTCTATGGAATGGAAGAGAGAGAGAGCCT 828
QY	358 GGCCTCTCATGATGATGGAACCATCAAAAGGAGAGAAAGAGAGACCAAGACCAAC 417
DB	829 CGCACTCTTTAATATGTGACCAACCAATGAGAGAGAGAGAGAGAGTGAACAGACCAAA 888
QY	418 GAAGAATGACATACCACTACCTAGAGATGTGATGAAGCCAGG--TATTAACT 474
DB	889 AAAAGGAAAAATTAATGTACCTGAAGATGTGATGAAGCCCAATGTGTTTTTAAACT 948

OY	475	TTGAAGACAGCCTCAGCGCACAAAAGTACTACAC	508
Db	949	TTGAAACACACCTTCATGCGACAAGAAGTATACAC	982
RESULT 9			
LOCUS	AX027005	972 bp	DNA
DEFINITION	Sequence 2 from Patent W00037102.		
ACCESSION	AX027005		
VERSION	AX027005.1	GI:10188040	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 972)		
AUTHORS	Rogers,N.J., Dorling,A. and Lechler,R.I.		
TITLE	Immunosuppression		
JOURNAL	Patent: WO 0037102-A 2 29-JUN-2000;		
	ROBERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;		
	LECHLER ROBERT IAN (GB)		
FEATURES	location/Qualifiers		
source	1..972		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	304 a	204 c	194 g
ORIGIN	270 t		
Query Match	41.8%; Score 212.6; DB 6; Length 972;		
Best Local Similarity	69.0%; Pred.No.5,5e-49;		
Matches	354; Conservative	0; Mismatches	144; Indels 15; Gaps 4;
OY	1	ATACAGATTACCCGAGAACCTAAGAGATGTATTTTCAGCTTAACACTGAGAAATTCACCT	60
Db	460	ATACAGGGTTACCAGCAACCTAAGAGAGAGTGTGTTTCCTAAGAACCAAGATTCACCT	519
OY	61	ACTAAGTATGATACGTGCATGTAAGAAATGTCAAAATTAATGTGACAGAACTGTACAAAGTT	120
Db	520	ATCGAGTATGATGTATTTATGCGAAATCTCAAGATAATGTACAGAACTGTACAGAGTT	579
OY	121	TCTATCAGCTGCCCTTTTTCAGTCCCCTGAAG--CACACATGTGAGCGTCTTTGTGCC	177
Db	580	TCCATCAGCTTGCTGTTTTCATTCCTCGATGTTAGAGCAATATGACCATCTTCTGTATT	639
OY	178	CTGAACACTGGAACACTGGAAGATGCTGCTCCCTACCTTCAATTAATATGACACAACT	237
Db	640	CTGGAAACTGACA--AGACGGCGCTTTATCTTCCCTTTCTTAATG-----AGCTT	690
OY	238	AAGGATTAAGACCCCTGGAACAAAGGCCACTTCCTGATGTGCGCTGACTTGTAAATGTTT	297
Db	691	GAGGACCCCTCAGCTCCCCAGACACATCTCTTGATTTACAGCTGTACTTCCAACAGTT	750
OY	298	GTTGTTTTTGTGGATGCTGCTTTTAAACACTAAGAAAAAGGGAAGAAGCAGCCT	357
Db	751	ATTATATGTGTATGGTCTTCTGCTAATTTCTATGGAATGGAAGAAGGAAGCGGCT	810
OY	358	GGCCCTCTCATGAAAGTGAATCAACATCAAAAGGAGAGAGAAAGAGCAACAGACCAAC	417
Db	811	CGCAACTCTTATTAATAGTGAACCAACAATGGAAGGGAAGAGTAGAACAGACCAAG	870
OY	418	GAAAGAGTACCTACCACTACCTGAGATGTGATGAGAGCCAGT---TATTAACATT	474
Db	871	AAAAGGAAAAATTCATATACCTGGAABATCTGATGGAAGCCAGGCTGTTTTTAAAGT	930
OY	475	TTGAAGACAGCCTCAGGCGACAAAGTACTACA	507
Db	931	TGGAAGACATCTTCATGCGACAAGTGTATACA	963

QY 421 AGAGTACCATACAGTACTGAGATCTGATGAAGCCAGTGTATTACATTTTGAAG 480
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Db 1143 AGAGTACCATACAGTACTGAGATCTGATGAAGCCAGTGTATTACATTTTGAAG 1202
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
|||||
Db 1203 ACAGCCTCAGGCGACAAAGTACTACACA 1231

RESULT 3
AF157827 1138 bp mRNA linear MAM 08-MAY-2000
LOCUS AF157827
DEFINITION Fc158 catinus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
ORGANISM
cat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
AUTHORS Chou, I.-S., Hash, S.M., Winslow, B.J. and Collisson, E.W.
TITLE Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
PUBMED 10713336
REFERENCE 2 (bases 1 to 1138)
AUTHORS Chou, I.-S., Hash, S., Winslow, B.J. and Collisson, E.W.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Km. 222, College Station, TX 77843, USA

FEATURES
source
1. .1138
Location/Qualifiers
/organism="Felis catus"
/db_xref="taxon:9685"
1. 1138
/gene="CD86"
63. .1052
/gene="CD86"
/note="B7-2 antigen"
/product="CD86 antigen"
/codon_start=1
/protein_id="AA042974.1"
/db_xref="GI:5381424"
/translation="MGICDSITGLSHLLVMAALLLSGVSSKSOAYFNKLGELPCHFT
NSONISLDELIVFWODQDLVLEYLRGENPONVLRKGRFSFDKNMTLRHNIQI
IKDGTGHCIFHYKGRGLVPMHOMSDLSVLANSOPETVTSNRTEGSLINLHVO
SIOGPEPKEMFOLNTEENSTKYDVMKSSONNVTLEYNVSISLSPSVPEANVSIFC
CALKIETLEMLSLPRNIIDQPKDKPEQSHFLMIAVLVMFVFCGMSFKTLRKRK
KKOPGSHCEETIKREKESKOTNERPVPHVPERSDACVNLTKTASGDKNO"

BASE COUNT 358 a 245 c 246 g 289 t
ORIGIN

Query Match 97.8%; Score 497.8; DB 4; Length 1138;
Best Local Similarity 99.6%; Pred. No. 4.7e-129;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATACAAGTTACCCAGACACTAAGAGATGATTTTTCAGCTAAACACTGAGATTCACT 60
|||||
Db 546 ATACAAGTTACCCAGACACTAAGAGATGATTTTTCAGCTAAACACTGAGATTCACT 605

QY 61 ACTAAGTATGATCTGCTGATGAGAAATTCAAAATATATGTGACAGAACTGTACAACTT 120
|||||
Db 606 ACTAAGTATGATCTGCTGATGAGAAATTCAAAATATATGTGACAGAACTGTACAACTT 665

QY 121 TCTATCAGCTTGCTCTTTTTCAGTCCCTGGAAGCACAAATGAGCGCTTTTGCCCTG 180
|||||
Db 666 TCTATCAGCTTGCTCTTTTTCAGTCCCTGGAAGCACAAATGAGCGCTTTTGCCCTG 725

QY 181 AAACCTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATAGATGACAACTAAG 240
|||||
Db 726 AAACCTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATAGATGACAACTAAG 785

QY 241 GATAAAGACCCCTGGAACAGGCGCACTTCCCTGGATTGCGGCTGTACTTGAATGTTGTT 300
|||||
Db 786 GATAAAGACCCCTGGAACAGGCGCACTTCCCTGGATTGCGGCTGTACTTGAATGTTGTT 845

QY 301 GTTTTGTGTGGAGTGTGCTCTTTTAAACACTAAGGAAAGAAAGAAAGACAGCTGGC 360
|||||
Db 846 GTTTTGTGTGGAGTGTGCTCTTTTAAACACTAAGGAAAGAAAGAAAGACAGCTGGC 905

QY 361 CCTCTCATGATGTGAACCATCAAAAGGAGAGAGAAAGACAAACAGCAAGAA 420
|||||
Db 906 CCTCTCATGATGTGAACCATCAAAAGGAGAGAGAAAGACAAACAGCAAGAA 965

QY 421 AGAGTACCATACACGTAAGTCTGAGATCTGATGAAGCCAGTGTATTACATTTTGAAG 480
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Db 966 AGAGTACCATACACGTAAGTCTGAGATCTGATGAAGCCAGTGTATTACATTTTGAAG 1025

QY 481 ACAGCCTCAGGCGACAAAGT 501
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Db 1026 ACAGCCTCAGGCGACAAAGT 1046

RESULT 4
AF106826 1897 bp mRNA linear MAM 14-DEC-1999
LOCUS AF106826
DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106826
VERSION AF106826.1 GI:6572516
KEYWORDS
SOURCE
dog.
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Yang, S. and Sim, G.K.
TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093996
REFERENCE 2 (bases 1 to 1897)
AUTHORS Yang, S. and Sim, G.-K.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA

FEATURES
source
1. .1897
Location/Qualifiers
/organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_type="peripheral blood mononuclear cells"
1. .1897
/gene="CD86"
1. .5
5' UTR
/gene="CD86"
6. .995
/gene="CD86"
/function="counter-receptor for CD28 and CD152 (CTLA4)"
/product="B7-2 protein"
/codon_start=1
/protein_id="AA171297.1"
/db_xref="GI:6572517"
/translation="MYLRCTMELNLIFFVMTLLLYGAASKSOAYFNKLGELPCHFTN
SONISLDELIVFWODQDLVLEYLRGENPONVLRKGRFSFDKNMTLRHNIQI
IKDGLYOCFVHFKGRGLVPMHOMSDLSVLANSOPETVTSNRTEGSLINLHVO
SIOGPEPKEMFVLTENSSTKYDVMKSSONNVTLEYNVSISLSPSVPEANVSIFC
VLOESMKLPSLPYNIIDHTAETPDGDHIIIMIAALVLMVILCGMVFETLRKRRKO
PGPSHECTMKVERKESRQTERVRYHETENSDEACVNIKSTASGDNSTTQF"

BASE COUNT 585 a 400 c 383 g 529 t
ORIGIN

Query Match 72.7%; Score 369.8; DB 4; Length 1897;
Best Local Similarity 85.7%; Pred. No. 4.1e-93;

FEATURES
source
Location/Qualifiers
1..2830
/organism="Felis catus"
/db_xref="taxon:9685"
1..2830
/gene="CD86"
179..1177
/gene="CD86"
/note="CD28/CTLA4 counter receptor; B7-2 protein"
/codon_start=1
/product="CD86"
/protein_id="AA03342.1"
/db_xref="GI:15418726"
/translation="MGICDSYMGSLHTLVALLSGVSSMKSOAYFNKGTGELPCHEFT
NSONTSLDELVEWODOKLYLVEIFRKGPNPOVHLKYKGRSPDKDNMTLRHNVO
IKDKGYHCFHFKPKGLVPMHOMSSDLSVLANSQPEITVSNRPNSTGILNITCS
SIQGPPEKREMYFQLTENSTYKDYTKMSSONNVTELVNYSISPEVPAHNVSE
CALKLETEMLISLPENIDAPKDPDQGHFLWIAVAVMFVFCGMSFKTLRKRK
KQPGPSHECETIKRERESKOTNERVPHVPERSDDEACINILKTASGDKSTTHF"
BASE COUNT 877 a 570 c 586 g 797 t
ORIGIN

Query Match 100.0%; Score 509; DB 4; Length 2830;
Best Local Similarity 100.0%; Pred. No. 3 4e-132;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGTAAACACTGAGAAATTCACCT 60
|||||
DB 662 ATACAGGTTACCCAGAACCTAAGAGATGTAATTTTCAGTAAACACTGAGAAATTCACCT 721
|||||
QY 61 ACTAGTATGATCGTATGTAAGAAATCTCAAAATATATGACAGAACTGTACACGTT 120
|||||
DB 722 ACTAAGTATGATCTGTATGTAAGAAATCTCAAAATATATGACAGAACTGTACACGTT 781
|||||
QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGGAACACACATGTGACGCTTTTGTGCCCTG 180
|||||
DB 782 TCTATCAGCTTGCCCTTTTTCAGTCCCTGGAACACACATGTGACGCTTTTGTGCCCTG 841
|||||
QY 181 AAACGTGGAACATGAGATGCTGCTCCTACCTTCAATATGATGACAACTAAG 240
|||||
DB 842 AAACGTGGAACATGAGATGCTGCTCCTACCTTCAATATGATGACAACTAAG 901
|||||
QY 241 GATAAAGACCTGGAACAGGCACTTCCTCGATGCGGCTGATCTGTAATGTTGTT 300
|||||
DB 902 GATAAAGACCTGGAACAGGCACTTCCTCGATGCGGCTGATCTGTAATGTTGTT 961
|||||
QY 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAAGAAAGAAAGCAAGCCTG 360
|||||
DB 962 GTTTTGTGGGATGCTGCTTTTAAACACTAAGAAAGAAAGAAAGCAAGCCTG 1021
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LOCUS AB030652
DEFINITION Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86),
complete cds.
ACCESSION AB030652
VERSION AB030652.1 GI:9796387
KEYWORDS B-lymphocyte activation antigen B7-2 (CD86).
SOURCE *Felis catus peripheral blood mononuclear cell cDNA to mRNA.
ORGANISM Felis catus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
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COMMENT
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SIQGPPEKREMYFQLTENSTYKDYTKMSSONNVTELVNYSISPEVPAHNVSE
CALKLETEMLISLPENIDAPKDPDQGHFLWIAVAVMFVFCGMSFKTLRKRK
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polyA_signal
BASE COUNT 378 a 281 c 260 g 351 t
ORIGIN

Query Match 99.7%; Score 507.4; DB 4; Length 1270;
Best Local Similarity 99.8%; Pred. No. 9.6e-132;
Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 696.962 Seconds
(without alignments)
15282.914 Million cell updates/sec

Title: US-09-646-561-30

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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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20: em_om:*
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23: em_pat:*
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32: em_htg_other:*
33: em_htgo_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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7	215.2	42.3	1044	9	AF344851		AF344851	Macaca ne
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9	212.6	41.8	972	6	AX027005		AX027005	Sequence
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LOCUS	AY007704				
DEFINITION	Felis catus CD86 (CD86) mRNA, complete cds.				
ACCESSION	AY007704				
VERSION	AY007704.1	GI:15418725			
KEYWORDS					
SOURCE					
ORGANISM	Felis catus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	1 (bases 1 to 2830)				
AUTHORS	Yang,S., Sellins,K.S., Powell,T., Stoneman,E. and Sim,G.K.				
TITLE	Novel transcripts encoding secreted forms of feline CD80 and CD86				
	costimulatory molecules				
JOURNAL	Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)				
PUBMED	21390213				
REFERENCE	2 (bases 1 to 2830)				
AUTHORS	Yang,S.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-SEP-2000) Immunology, Heska Corporation, 1613				
	Prospect Parkway, Ft Collins, CO 80525, USA				

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Job time : 44.5402 secs

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RESULT 15
US-08-702-525-24
Sequence 24, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopolo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1134
US-08-702-525-24

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Best local similarity 75.4%; Pred. No. 1,5e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

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QY 377 AATGAGTTTCACTGATGATGCTGTCTGCTACTGATGATCACTGATCACTGATCACTGAT 436
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Db 828 CTGCCCCAAGCAGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 887
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RESULT 14
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; Sequence 24, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nalder, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules

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; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCE: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 148..1134
; US-08-205-697A-24

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Query Match 54.28; Score 540; DB 4; Length 1161;
Best Local Similarity 75.48; Pred. No. 1.5e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

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QY 77 CCAATGAGAGTCAAGCATATTTCACAAAGAGTGGAGTGGCCATGATTTTCAAACT 136
Db 221 CTGGAAGATTCAGACTTATTTCAATGAGACTGACAGCTGCCATGCAATTTGCAAACT 280
QY 137 CTCGAAGATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
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QY 377 AATGAGTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436
Db 521 AGATGAAATTCGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 580
QY 437 CTAAATGAGACAGAAATTTGCGCATCAATAATTTGAGCTGCTCATCTATCAAGAGTTACC 496
Db 581 CTAAATGAGACAGAAATTTGCGCATCAATAATTTGAGCTGCTCATCTATCAAGAGTTACC 637
QY 497 CAGAACCTTAAGAGATGATTTTCACTTAACACTGAGAAATTCACATTAAGATGATGATA 556

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;
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08--403-253A-3

Query Match          54.2%; Score 540; DB 4; Length 1120:
Best Local Similarity 75.4%; Pred. No. 1.4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

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DB 120 GCACATGAGGAGTGAAGTCACTCTCTCTGATGAGCCCTGCTCTGCTGTTCTT 179
QY 77 CCATGAGAGTCAAGCATTTTCAACAGAGCTGAGAACTGCCATTTTACAAACT 136
DB 180 CTTCTGAGAGTTCAGCTTATTTCAATGAGAGCTGCAGACCTGCCATTTTCAAACT 239
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DB 240 CTCAAACATTAAGCCGTGAGCTGAGTATTTTGGAGAGCAGAGATAAGCTGCTC 299
QY 197 TGTATGAGATTTTCAGAGGCAAGAGAAACCTCAAAATGTCATTCAAATTAAGGCGC 256
DB 300 TGAATGAGGATTAAGTGAAGCAAGAAATTTGACAGTGTTCATTCAGATATAGGGCC 359
QY 257 GTACAGCTTTTACAGAGCAAGCAAGTGCAGCTCCACATTTTACATCAAGAGACA 316
DB 360 GCACAGATTTTATTCGCGACAGTGGACCTTGACATTCACAAATTCAGATCAAGAGACA 419
QY 312 AGGGACATATCACTGTTTCATTTCAATTAAGGGCCCAAGGACTACTTCCATGACAC 376
DB 420 AGGGCTTGATCAATGATATCAATCAATCAAAAGCCCAAGGAAATGATGCAATCCAC 479
QY 377 AAATGAGTTTACCTATACAGTGTCTTGTCTTACCTGATCACTGATTAACAGTAACT 436
DB 480 AGATGAAATTCGAACTGTCAGTGTCTTGTCTTACCTGATCACTGATTAACAGTAACT 539
QY 437 CTAATGAGCAAGAAATTCGTGCATCATTAATTTTACCTGCTCATCTATACAGGTTACC 496
DB 540 CTAATGAGCAAGAAATTCGTGCATCATTAATTTTACCTGCTCATCTATACAGGTTACC 596
QY 497 CAGAACCTAAGAGATGATTTTTCAGCTAAACACTGAGATTCACCTCAAGTATGATA 556
DB 597 CAGAACCTAAGAGATGATTTTTCAGCTAAACACTGAGATTCACCTCAAGTATGATA 656
QY 557 CTGTCATGAGAAATCTCAAAATATGACAGAACTGTACAGCTTCTATCAGCTTGC 616
DB 657 GTATATGACAGAAATCTCAAGATATGTCACAGAACTGTACAGCTTCTATCAGCTTGT 716
QY 617 CTTTTCAGTCCCTGAGAG---CACACAATGTGAGCGCTTTTGTGCCCTGAAAGCTGAGA 673
DB 717 CTGTTTCATTTCTGATGTTTACGAGACATATGACCATCTCTGATTTGGAAGTGAACA 776
QY 674 CACGTGAGATGCTGCTCCCTACCTTCATATAGATGACCAACCTTAAGATTAAGACC 733
DB 777 ---AGACGGGCTTTTATCTTACCTTCTCTATAG-----AGCTTGAGAGACCTCAGC 827
QY 734 CTGAACAAGGCACTTCTCTGATTTGGGCTGTACTGTAATGTTTGTGTTTGTG 793
DB 828 CTCGCCAGACCAATTCCTTGTGATTCAGCTGTACTTCCAAACAGTTATTTATGTGGA 887
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QY 794 GGATGCTGTCTCTTAAACACTAAGAAAGAGAAAGCAAGCCCTGCCCCCTTCATG 853
DB 888 TGGTTTCTGCTTAATTCATATGAAATGAGAAAGAAAGAGCGGCTCGCAACTATATA 947
QY 854 AATGTGAACCATCAAAAAGGAGAGAAAGAGACCAACGACCAAGCAAGAGTACCAT 913
DB 948 AATGTGAACCCACACATATGAGAGAGAGAGAGTGAACGACCCACAAAGAGAAAAA 1007
QY 914 ACCAGTACCTGAGAGATCTGATGAGCCAGTG---TATTACATTTTGAAGACACCT 970
DB 1008 TCCTATATCCGTAAGATCTGATATCAAGCCAGCGTGTTTTAAAGTTCCAAAGACATCTT 1067
QY 971 CAGCGACAAAAGTACTACACATTTT 996
DB 1068 CATCGACAAAAGTATACATGTTT 1093

RESULT 13
PCT-US95-02576-22
; Sequence 22, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF INVENTION: and Uses Therefor
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; PCT-US95-02576-22

Query Match          54.2%; Score 540; DB 5; Length 1120:
Best Local Similarity 75.4%; Pred. No. 1.4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACATGAGGAGTGAAGTCACTCTCTGATGAGCCCTGCTCTGCTGTTCTT 76
DB 120 GCACATGAGGAGTGAAGTCACTCTCTGATGAGCCCTGCTCTGCTGTTCTT 179
QY 77 CCATGAGAGTCAAGCATTTTCAACAGAGCTGAGAACTGCCATTTTACAAACT 136
DB 180 CTTCTGAGAGTTCAGCTTATTTCAATGAGAGCTGCAGACCTGCCATTTTCAAACT 239
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Db      1068 CATGCCACAAAGTATGATTACTTTT 1093
|||||
RESULT 10
US-08-205-697A-22
Sequence 22, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
Applicant: Sharpe, Arlene H.
Applicant: Borriello, Francescopaulo
Applicant: Freeman, Gordon J.
Applicant: Nadler, Lee M.
Title Of Invention: NO. 6218510el Forms of T Cell Costimulatory Molecules
Title Of Invention: and Uses Therefor
Number Of Sequences: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
Application Number: US/08/205,697A
Filing Date: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
Registration Number: 36,207
REFERENCE/DOCKET NUMBER: BVI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-205-697A-22

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Query Match	54.28;	Score 540;	DB 4;	Length 1120;
Best Local Similarity	75.48;	Pred. No. 1,4e-160;		
Matches 743;	Conservative	0;	Mismatches 225;	Indels 18;
			Gaps	5;

QY	17	GCACATAGGAGCATAGTCACACTCTCCTTGTGATGGCCCTCTGCTGCTGGTGTCTT	76
Db	120	GCACATAGGAGCATAGTACACTCTCTTTGTGATGGCCCTCTCTCTCTGTGCTGCTC	179
QY	77	CCATGAGAGTCAAGCATATTTCAACAGACTGGAGAACTGCCATTTTACAAACT	136
Db	180	CTTGAGAGATTCAGAGCTATTTCAATGAGACTGCAGACTGCCAATTTGGAACCT	239
QY	137	CTCAAAACATATGACCTGGATGAGCTGCTGATGATATTTTGGCAGACCAGATGAGCTGTTTC	196
Db	240	CTCAAAACCAAGGCTGAGTGGCTAGTAGATATTTTGGCAGAGACAGGAAACTGGTTTC	299
QY	197	TGTATGATATTTTCAAGGCGCAAGAGAACTCTCAAAATGTTCAATCTCAAAATATAGGCC	256
Db	300	TGAATGAGATTACTATGGCGCAAGAGAAATTTGCAGATGTTCAATTCGAATATATGGGCC	359
QY	257	GTCACAGCTTTGACAAAGGACACCTGAGCCCTGAGAGCTCCAAATGTTCAATATCAAGAGCA	316
Db	360	GCACAGATTTTGAATTCGAGACGTTGGACCTCGAAGATTTCAAAATCTTCAGATCAAGAGCA	419

QY	317	AGCACAAATACACTGTTTATTCATATATTAAGGGCCAAAGACACTAGTCCATGCAC	376
Db	420	AGGGCTTGATCAATGTATATCATCATCACAAGAGCCACAGGAATGATTCGATCCAC	479
QY	377	AAATGAGTCTGACCTTATCATGCTGCTGCTCACTTCACTAGTAACCTGAAATACAGTAAC	436
Db	480	AGATGAATTCGAACTGTCAAGTGGCTTGCTAACTTCAGTCAACCTGAATATGACCAATT	539
QY	437	CTAATGAACAGAAAATTCGGCATATTAATTTGACCTGCTCATCTATACAAAGTTAC	496
Db	540	CTAATATPACGAAAA--TGCTGACTTAATTTGACCTGCTCATATCATACGGTTAC	596
QY	497	CAGAACCTAAGSAGATATTTTCAGTCAACACTAGATACTCACTAGTATGATA	556
Db	597	CAGAACCTAAGSAGATATGAGTGGTTGGTAGAACCAAGAATTCACTATCAGATATGAG	656
QY	557	CTGTCATGAAAGAATCTCAAAATATATGTGACAGACTGTACAACTGTTTATACGCTTC	616
Db	657	GTAATATATGCAAAATCTCAAGATTAATGTCAACAACTGACAGCTTTTCAATCAGCTGT	716
QY	617	CTTTTCAGTCCCGGANG---CACACAATGTAGGCGCTTTGTGGCCCTGAATCGAGA	673
Db	717	CTGTTTATTCGCCGATGATGTACGACGAATATGACCACTTTCTGTATTCGTGAAACTGAC	776
QY	674	CACGTGAGATGCTGCTCTCCCTACCTTTCATATATGAGTGCACAACTGAGATAAAGCC	733
Db	777	---AGACGGCGCTTTTATCTTCACCTTTCCTATAG-----AGTTGAGGACCTCCAGC	827
QY	734	CTGAACACAGGCACTTCCTCTGTGATGGCGGCTGACTTGTAATGTGTTGTTTTTG	793
Db	828	CTCCCCAGACACATCTCTTGATTTACAGCTATCTTCCAAAGTATATATATGTGGA	887
QY	794	GGATGATGTCCTTTAAAACTAAGAAAAAGAAAGAGACAGCCCTGCGCTCTCATG	853
Db	888	TGCTTTTCTGTCTAATTCATGTGAAATATGAGAAGAAAGCGGCTCCCACTCTTATA	947
QY	854	AATGTGAACCATCAAAAAGGAGAGAAAAAGAGCAACACAGCAAGAAAGATGCAT	913
Db	948	AATGTGAACCAACACATGAGAGAGAGAGAGAGTGTACACAGCAAGAAAGAGAAAAA	1007
QY	914	ACCACTACCTGAGAGATCTGATGAGAGCCAGTG---TATTAACTTTTGAAGACAGCT	970
Db	1008	TCCATATACCTGAAAGATCTGATGAGAGCCAGCGTGTTTTAAAGTTGAAGACATCTT	1067
QY	971	CAGCGCAAAAAGTACTACACATTTT	996
Db	1068	CATCGCAAAAAGTATGATCACTGTTT	1093

RESULT 11
 US-08-702-525-22
 : Sequence 22, Application US/08702525
 : Patent No. 6294660
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Sharpe, Sharpe
 : APPLICANT: Borriello, Francescopolo
 : APPLICANT: Freeman, Gordon
 : APPLICANT: Nadler, Lee
 :
 : TITLE OF INVENTION: No. 62946601 Forms of T Cell Costimulatory
 : TITLE OF INVENTION: Molecules and Uses Therefor
 :
 : NUMBER OF SEQUENCES: 65
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: LAHIVE & COCKFIELD
 : STREET: 28 State Street
 :
 : City: Boston
 :
 : STATE: Massachusetts
 :
 : COUNTRY: USA
 :
 : ZIP: 02109-1875
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS

Db 777 ---AGAGCGGCTTTATCTTCACTTTCTCTATAG-----AGCTTGAGAGCCCTCAGC 827
QY 734 CTGAACAAGGCCACTCTCTCTGATTCGGCTGCTACTGTATGTTTGTGTTTGTG 793
Db 828 CTCGCCAGACACATCTCTTGATTAACACTGACTTCAACAGTTATATATGTGTA 887
QY 794 GGATGCTGCTTTAAACCTAAGGAAAGAAAGAACGACGCTGGCCCTCTCAG 853
Db 888 TGGTTTCTCTTAATTCATGGAATGGAAGAAAGGCGCTCGCACTCTTATA 947
QY 854 AATGTGAACCATCAAAAGAGAGAAAGAGCAACAGACCAAGAGAGTACCAT 913
Db 948 AATGTGAACCAACACATGAGAGAGAGAGAGTACAGACCAAGAAAGAGAAAAA 1007
QY 914 ACCAGCTAGCTGAGATCTGATGAAGCCCAAGT--TATTAACATTTGAGACAGCT 970
Db 1008 TCCATATACCTGAAGATCTGATGAAGCCAGCGCTTTTAAAGTTGAAGACATCTT 1067
QY 971 CAGCGCAAAAGTACTACATTTT 996
Db 1068 CAGCGCAAAAGTACTACATTTT 1093

RESULT 9

US-08-280-757B-1

; Sequence 1, Application US/08280757B

; Patent No. 6130316

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; APPLICANT: Gray, Gary S.

; APPLICANT: Greenfield, Edward

; TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/280,757B

; FILING DATE: 26-JUL-1994

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/101,624

; FILING DATE: 26-JULY-1993

; APPLICATION NUMBER: 08/109,393

; FILING DATE: 19-AUG-1993

; APPLICATION NUMBER: 08/147,773

; FILING DATE: 3-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-004CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1120 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-280-757B-1

Query Match 54.2%; Score 540; DB 3; Length 1120;
Best Local Similarity 75.4%; Pred. No. 1,4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCATATGAGAGTGGTGCACACTCTCTTGTGATGGCCCTCTGCTCTGTTCTT 76
Db 120 GCATATGAGAGTGGTGCACACTCTCTTGTGATGGCCCTCTGCTCTGTTCTT 179
QY 77 CCATGAAGAGTCCAAACATATTTCAACAGACTGGAACCTGCCATTTTCAAACT 136
Db 180 CTTGTAAGATTCACACCTATTTCATGAGACTGCAGACCTGCCATTTTCAAACT 239
QY 137 CTCAAACATTAAGCTGGATGAGCTGGTATGTTTGGCAGAGCAGATTAAGCTGTT 196
Db 240 CTCAAACCAAGCCCTGAGTATGATGATTTTGGCAGAGCAGAAACCTTGGTTTC 299
QY 197 TGTATGATATATTCAGAGCAAGAACCTCAAAATGTCATCTCAATATTAAGGCC 256
Db 300 TGAATGAGTATACTTAGGCAAGAAATTTGACAGTGTTCATTCAGATATATGGGCC 359
QY 257 GTACAGCTTTGACAGAGACAACTGACCTGAGACTCCACAAATGTTTCAGATCAAGACA 316
Db 360 GCACAAAGTTTATGATCGGACAGAGTGGACCTGAGACTTCACAACTTCAGATCAAGACA 419
QY 317 AGGCAACATATCACGTTTCATTCATTTAAAGGCCCAAGAGACTAGTTCCCATGACC 376
Db 420 AGGCTTGTATCAATGATCATCATCAACAAAGCCACAGGATATATGCAATCCAC 479
QY 377 AAATAGTTTGACCTATCATGCTTGTGTAACCTTCACTCAACCTGAATAACACTACTT 436
Db 480 AGATGAATTCGACCTGACATGCTGCTGCTTACTTCACTCAACCTGAATAACACTACTT 539
QY 437 CTAAATGACAGAAATTCCTGACATCATTAATTTGACCTGCTCATATACAGGTTACC 496
Db 540 CTAAATGACAGAAATTCCTGACATCATTAATTTGACCTGCTCATATACAGGTTACC 596
QY 497 CAGAACCTAAGAGATATTTTTCAGTAAACCTGGAATTCAGTAAATTAAGATGATA 556
Db 597 CAGAACCTAAGAGATGAGTGTGTTTGTCTAAGAACCAAGATTCAGTAAATTAAGATG 656
QY 557 CTGTCATGAGAAATCTCAAAATATATGACAGAACTGTACAAAGTTTCTATCAGCTTGC 616
Db 657 GTATATGACAGAAATCTCAAAATATATGACAGAACTGTACAAAGTTTCTATCAGCTTGC 716
QY 617 CTTTTCAGTCCCTGAG--CACACAAATGAGCGCTTTTGTGCTGAACTGAGAGA 673
Db 717 CTTTTCAGTCCCTGAGTATGAGCAATATGACCAATATGATCTGTGAAACTGACA 776
QY 674 CACTGAGATGCTGCTCCCTACCTTTCATTAATGATGACCAACTAAGATTAAGATG 733
Db 777 ---AGAGCGGCTTTATCTTCACTTTCTCTATAG-----AGCTTGAGAGCCCTCAGC 827
QY 734 CTGAACAAGGCCACTCTCTCTGATTCGGCTGCTACTGTATGTTTGTGTTTGTG 793
Db 828 CTCGCCAGACACATCTCTTGATTAACACTGACTTCAACAGTTATATATGTGTA 887
QY 794 GGATGCTGCTTTAAACCTAAGGAAAGAAAGAACGACGCTGGCCCTCTCAG 853
Db 888 TGGTTTCTCTTAATTCATGGAATGGAAGAAAGGCGCTCGCACTCTTATA 947
QY 854 AATGTGAACCATCAAAAGAGAGAAAGAGCAACAGACCAAGAGAGTACCAT 913
Db 948 AATGTGAACCAACACATGAGAGAGAGAGAGTACAGACCAAGAAAGAGAAAAA 1007
QY 914 ACCAGCTAGCTGAGATCTGATGAAGCCCAAGT--TATTAACATTTGAGACAGCT 970
Db 1008 TCCATATACCTGAAGATCTGATGAAGCCAGCGCTTTTAAAGTTGAAGACATCTT 1067
QY 971 CAGCGCAAAAGTACTACATTTT 996

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OY 437 CTAATGAAAGAAAATTCGGCATCTAAATTTGACCTGCATCTATACAAAGTTACC 499
Db 540 CTAATATACAGAAA---TGTGACATTAATTTGACCTGCTCATCTATACAGGGTTACC 596
OY 497 CAGAACCTAAGAGATGTATTTTCAGCTAAACACTGAGATTCACCTACTAAGTATGATA 556
Db 597 CAGAACCTAAGAGATGTATTTTCAGCTAAACCAAGATTCACCTACTAAGTATGATA 656
OY 557 CTGTCATGANAATAATCTCAAAATTAATGTACACAACTGACACCTTTCTACAGCTGAC 616
Db 657 GTATTATGCAAAATCTCAAGATTAATGTACACAACTGACACCTTTCTACAGCTGAC 716
OY 617 CTTTTCAGTCCCTGAAG---CACACAAATGTGACCGCTTTTGTGCCCTGAACCTGGAGA 673
Db 717 CTGTTTCATTTCCGTGATGTTTACGACGAATATGACCATCTCTGTATTCGGAACCTGACA 776
OY 674 CACTGGAGATCTCTCTCCCTACCTCTTCAATATAGATGCACAACTAAGGATTAAGACC 733
Db 777 ---AGACCGGCTTTTATCTTACACCTTTCCTATAG-----AGCTTGGAGACCCCTCAC 827
OY 734 CTGAACAAGGCGCACTTCCTCGATGATGCGGCTGACCTGTGATATGTTGTGTTTTGTG 793
Db 828 CTCCCCGAGACCAATTCCTTGATTTACACTGTACTCTCAACAGTATTTATATGTGTGA 887
OY 794 GGATGTGTCTCTTTAAAAACACTAAGAAAAGAAAGAACGACCTGTGCCCTCTCATG 853
Db 888 TGGTTTCTGTCTAATTCATATGAAATATGAAAGAAAGAACGCGCTCCCACTCTTATA 947
OY 854 AATGTGAACCATCAAAAAGGAGAGAAAGACAAACAGACCAAGCAAGATACAT 913
Db 948 AATGTGAGAACCAACATATGAGAGGAGAGAGATGACAGACCAAGAAAGAGAAAAA 1007
OY 914 ACCACGTACCTGAGAGATCTGATGAAGCCCAAGT---TATTAACTTTTGAAGACAGCCT 970
Db 1008 TCCATTTATACCTGAAGAAGATGTGATGAAGCCCAAGGCTGTTTAAAGTTGGAAGACATCTT 1068
OY 971 CAGCGCAAAAAGTACTACACATTTT 996
Db 1068 CATGCGAACAAAAGTACTACATGTTT 1093

RESULT 8
US-08-479-744A-1
: Sequence 1, Application US/08479744A
: Patent No. 6084067
: GENERAL INFORMATION:
: APPLICANT: Freeman, Gordon J.
: APPLICANT: Nadler, Lee S.
: APPLICANT: Gray, Gary S.
: TITLE OF INVENTION: No. 6084067el CTIL4/CD28 ligands and
: TITLE OF INVENTION: Uses Therefor
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/479,744A
: FILING DATE: June 7, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/280,757
: FILING DATE: 26-JUL-1994
: APPLICATION NUMBER: 08/109,393
: FILING DATE: 28-AUG-1993

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	APPLIATION NUMBER: 08/101,624	
	FILING DATE: 26-JULY-1993	
	APPLICATION NUMBER: 08/147,773	
	FILING DATE: 3-NOV-1993	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Mandragouras, Amy E.	
	REGISTRATION NUMBER: 36,207	
	REFERENCE/DOCKET NUMBER: RPI-004CP3	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (617) 227-7400	
	TELEFAX: (617) 227-5941	
	INFORMATION FOR SEQ ID NO: 1:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 1120 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	MOLECULE TYPE: cDNA	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: 107..1093	
	US-08-479-744A-1	
	Query Match	54.2%; Score 540; DB 3; Length 1120;
	Best Local Similarity	75.4%; Pred.No.1,4e-160;
	Matches 743; Conservative	0; Mismatches 225; Indels 18; Gaps
Oy	17 GCACATAGTGGACTGTCGTACACTCCTTGATGGCCCTCGCTCTGCTGTTCTT	76
Dd	120 GCACATATGGACTAGTAACTTCTTTTGATBGCCTTCTGCTCTGTGCTGCTC	178
Oy	77 CCATAGAGAGTCAMGCATATTTTCAACAAGACTGGAGAAGCTGCCATTCATTTCAA	136
Dd	180 CTCGTGAATTCACACTATTTCATGTAGAGCTGCAGACTCCATGTGCCAATTTCCA	238
Oy	137 CTCAAAACATAAGCCTGSATAGCTGCGTAGATTTTGGCAGAGACCAGATTAAGCTG	196
Dd	240 CTCAAAACCAAGCTGTAGTGTAGTATTTTGGCAGAGACCAGAAAACCTTGCTTC	298
Oy	197 TGTATGATATATTACAGAGCAAGAACCCCTCAAAATGTTTCATCTCAAAATTAAG	255
Dd	300 TGAATGAGGTATTTAGGCAAGAAATTTGACAGTGTTCATTCAGATATATGGGCC	358
Oy	257 GTACAACTTTGACAGAGCAACTGACCTGAGACTCCAAATGTTCAAGATCAAGACA	316
Dd	360 GCACAAAGTTTGATTCGAGACGTTGACCTGAGACTTCACAACTTCAGATCAAGACA	418
Oy	317 AGGCAACATATCACGTGTTTCATTCATTATTAAGGGCCCAAGGAGCTAGTTCCATG	376
Dd	420 AAGCGTTGATCAATGATCATTCATCAAAAAAGCCACAGGATGATGATTCATCCAC	478
Oy	377 AAATAGTTCTGACCTATCAGTGTCTGCTAACTTCAGTCAACCTGAAATTAACAGT	435
Dd	480 AGATTAATTCAGATGTCAGATGCTTGTCTTAACTTCAGTCAACCTGAAATTAACAGT	538
Oy	437 CTAATGAAAGCAAAATTCGTGGCATCAATAATTTGACCTGCTCATATACAGGTTAC	496
Dd	540 CTAATATACAGAAA--TGTGTACATTAATTTTGACCTGCTCATATACAGGTTAC	598
Oy	497 CAGAACCTAAGAGATGATTTTTCAGCTAAACACTGAGAAATTCACATAGATATATA	556
Dd	597 CAGAACCTAAGAGATGATGTTTTTGTGCTAAGAACCAAGAAATTCACATAGATATG	658
Oy	557 CTGTGATCAAGAAATCTCAAAATTAATGTGACAGAACTGTACAGCTTTCTATCAGCT	616
Dd	657 GTATATATCAAAATCTCAAAATTAATGTGACAGAACTGTACAGCTTTCTATCAGCT	718
Oy	617 CTTTTCAGTCCCGAAG--CAACATGTGAGCGCTTTTGTGGCCTGAAACTGAGA	675
Dd	717 CTGTTTCTTCTGATGTTTACGAGCAATATGACCATCTTCTGTATTTCTGAAACTGACA	778
Oy	674 CACTGGAAATGCTGCTCCCTACCTTTCATATAGATGCAACAACCTAAGATTAAGACC	735

OY	77	CGGGAAGAGTCAGCAATATTTTCACAAAGACTGGAAGACTGCCATGCCATTTTACAAC	136
Db	180	CTGTGAAGATTCACCTTATTTTCATGAGACTGAGACCTGCCATGCCATTTTGCAAC	239
OY	137	CTCAAAACATTAAGCGCTGGATGAGCTGGTAATTTTGGCAGGACCCAGATTAAGCTGGTTC	196
Db	240	CTCAAAACCAAGCGCTGAGTGAAGCTAGTAATTTTGGCAGGACCCAGATTAAGCTGGTTC	299
OY	197	TGTATGAGATTTTGAAGGCAAGAGAACCCCTCAAAATGTTCAATATATTAAGGGCC	256
Db	300	TGAATGAGGTACTTATAGGCAAAAGAAATTTTACAGTGTTCATTCCTCAAGTATATGGGCC	359
OY	257	GTACAGGTTTGACAAGGACAACTGGACCGCTGGACCTCCACATGTTTCAGATCAGGACA	316
Db	360	GCACAGTTTGGATTGGCAGAGTTGGACCGCTGGAGACTTCAAACTTCAGATCAAGGACA	419
OY	317	AGGGCACAATATCACTGTTTCAATTCATATATTAAGGGCCCAAGAGCATAGTTCCCATGCC	376
Db	420	AGGGGTTGTATCATATGATATCATCATCATCAAAAAGCCCAAGGAATGATTCGATCCACC	479
OY	377	AAATGAGTTCTGACCTATACAGTGGCTTGTCTAAGTTCAGTCAACTGGAATTAACGTAAT	436
Db	480	AGATGAATCTGAAGCTGACGTGGCTTGTCTAAGTTCAGTCAACTGGAATTAAGTACCAAT	539
OY	437	CTAATAGACGAATTAATTTGGCATCACTAAATTTGACCGCTGCATCTATTAACAAGTTACC	496
Db	540	CTAATATTAACGAATA--TGTGTACATATAATTTGACCTGGCTCATATTAACAAGTTACC	596
OY	497	CAGAACTTAAGAGATGATATTTTACGTAACAACACTGGAATTAACACTAAGTATGATA	556
Db	597	CAGAACTTAAGAGATGATGAGTGTGTGTGAAGAACCAAGATTTCACTATCGATGATGATG	656
OY	557	CTGTATGAGAAATTTTCAAAATATGTTGACAGAACTGTACAAGTTTCTATCAGCTTGC	616
Db	657	GTATATGACAAATTTCTCAGATATGCTCAGAACTGTACAGACGTTTCCATCAGCTTGT	716
OY	617	CTTTTTCAGTCCCGAAG--CACACAGATGAGCGCTTTTGTGCCCTGAACCTGAGAA	673
Db	717	CTGTTTCACTTCCGTGAATGTTACGAGCAATATGACCACTTCTGTATTTGGAACATGACA	776
OY	674	CACGTGAGATCTGCTCTCCCTACCTTCAATATAGTACACAACTTAAGATTAAGAAC	733
Db	777	---AGAGCGGCTTTTATCTTCAACCTTCTCTATAG-----AGCTTGAAGACCTCAGC	827
OY	734	CTGAACAGGCGCACTTCTCTGTGGATGCTGGCTGTACTTGTATGTTTGTGTTTTGTG	793
Db	828	CTCCCCAGACACATCTCTTGGATTAACAGCTGTACTTCCAACAGTTATATATATGTTGA	887
OY	794	GGATGCTGTCTTTAAACACATAAGGAAAGAAAGAAAGAACAGCGCTGGCCCTCTCATG	853
Db	888	TGTTTTCTGTCTAATCTCTATGGAATATGAAAGAAAGAAAGCGGCTCTCAACTCTTATA	947
OY	854	AATGTGAACCATCAAAAGGAGAGAAAGAGAACAGACCAAGACAGAAAGATGATCCAT	913
Db	948	AATGTGAACCAACCAATGAGAGAGAGAGAGAGAGTGAACAGACCAAGAAAGAGATAAAA	1007
OY	914	ACCAAGTACTGAGAGATCTGATGAAGCCCAAGT---TATTAACATTTTGAAGACAGCT	970
Db	1008	TCCATATATACCGAAGATCTGATGAAGCCCAAGGCTGTTTTTAAAGTTGGAAGACATCT	1067
OY	971	CAGCGCAAAAGTACATCAATTTT	996
Db	1068	CATCGACAAAGTACATCAATTTT	1093

RESULT 7
US-08-101-624-1
; Sequence 1, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.

```

1  TITLE OF INVENTION: No. 5942607e1 CTRAA/CD28 Ligands and
2  TITLE OF INVENTION: Uses therefor
3  NUMBER OF SEQUENCES: 25
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: LAHIVE & COCKFIELD
6  STREET: 60 State Street, Suite 510
7  CITY: Boston
8  STATE: Massachusetts
9  COUNTRY: USA
10 ZIP: 02109
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/101,624
19 FILING DATE: 26-JUL-1993
20 CLASSIFICATION: 514
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:
23 FILING DATE:
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Mandragouras, Amy E.
27 REGISTRATION NUMBER: 36,207
28 REFERENCE/DOCKET NUMBER: RPI-004
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (617) 227-7400
31 TELEFAX: (617) 227-5941
32 INFORMATION FOR SEQ. ID NO.: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 1120 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: cDNA
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 107..1093
42 US-08-101-624-1

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	Query Match	54.2%	Score 540	DB 2	length 1120
	Best Local Similarity	75.4%	Pred. No. 1,4e-160		
	Matches 743	Conservative	0	Mismatches 225	Indels 18
				Gaps	5
QY	17 GCATATGAGACAGAGTCACACTCTCTCTGTATGAGGCCCTCTCTCTCTGATGTTTCTT	76			
Db	120 GCATATGGGACAGATACATCTCTTTGTATGGCTTCTCTCTCTCTGATGTTCTCTC	179			
QY	77 CCATGAAGAGTCACAGCATATTTCCAAACAGCTGGAACTGCCATGCCATTTTCAAACT	136			
Db	180 CTCGGAAGATTCAAGCTTATTTCAATGAGACGCGAGACCTCCATGGCAATTTGCCAACT	239			
QY	137 CTCAAAACATTAACCCCTGGATGAGCTGGTGTATTTTGGCAGACACAGAAATAGCTGTTTC	196			
Db	240 CTCAAAACCAACCTCTGAGTGAAGCTAGTATTTTGGCAGACACAGAAATAGCTGTTTC	239			
QY	197 TGTATGATATTTACAGAGCCAAAGAAAGAACCCCTCAAAATGTTTCATCTCAAAATATATAGGCC	256			
Db	300 TGAATGAGTATCTATGAGCAAAAGAAATTTGACAGTGTTCATTTCCAAAGTATATGGCC	359			
QY	257 GTCAACACTTTGACCAAGGCAACACTGGACCTTGAGACTCCAAATGTTCAAGTCAAGGACA	316			
Db	360 GCACAAATTTTGTATGGACAGTGTGACCCCTGAGCTTCACAAATCTTCAGATCAAGGACA	419			
QY	317 AGGCGACATATCTACTTTTCATTTATATAAAGGGCCCAAGAGACTGATTTCCATGACAC	376			
Db	420 AGGGCTTGTATCAATATATCATCATCAACAAAAGCCCAAGAAATATTTTCGATCCACG	479			
QY	377 AAATGATCTGACCTATCATGCTGTCTGTAACTTCAGTCAACTGGAATATACAGTAACTT	436			
Db	480 AGATATGATTTCTGAACTGTCAAGTGTGTTGTAATTCAGTCAACCTGGAATATGTCACAACTT	539			


```

? APPLICANT: Sprent, Jonathan
? APPLICANT: Brunmark, Anders
? APPLICANT: Jackson, Michael
? APPLICANT: Peterson, Per A
? TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
? TITLE OF INVENTION: ACTIVATION OF T-CELLS
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Olsson & Hierl, Ltd.
? STREET: 20 No. 6251627th Wacker Drive, Suite 3000
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentln Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/039,641
? FILING DATE: 8-MAR-1995
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Olsson, Arne M.
? REGISTRATION NUMBER: 30,203
? REFERENCE/DOCKET NUMBER: T5R14710
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 580-1180
? TELEFAX: (312) 580-1189
? INFORMATION FOR SEO ID NO: 33:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1002 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? US-09-039-641-33

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Query Match          54.2%; Score 540; DB 4; Length 1002;
Best Local Similarity 75.4%; Pred. No. 1.3e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACRTAGGAGTGTGACACTCTCTCTGATGGCCCTCCTGCTCTGCTGTTCTT 76
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DB 20 GCACRTATGGAGTGTGACACTCTCTCTGATGGCCCTCCTGCTCTGCTGCTC 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 77 CCATGAAGTCAAGCATATTTCAACAGAGTGGAGAACTGGCATGCTTTTCAACT 136
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 80 CTCGTAGAGTTTAAAGCTTATTTCAATGAGACTGACAGCTGCCATGCCAATTTGCAACT 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 137 CTCAAACATAAGCCTGATGAGTGTAGTATTTTGGCAGAGCAGAGATAGCTGTTTC 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 140 CTCAAACCAAGCCTGAGTGTAGTATTTTGGCAGAGCAGAGAAACTTGGTTTC 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 197 TGTATGAGATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCTCAATTAAGGGCC 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 200 TGAATGAGGTATCTTAGGCAAAAGAAATTTGACAGTGTTCATCTCAAGTATAGGGCC 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 257 GTACAAGCTTTGACAAGGCAACTGGACCTGAGACTGCACATGTTCAAGTCAAGGCA 316
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 260 GCACAGATTTTATTCGGACAGTTGGACCTGAGACTTCACAAATCTTAGATCAAGGCA 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 317 AGGCAACATATCTGTTTCATCTTAATAAGGGCCCAAGAGCTAGTTCCTGACAC 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 320 AGGGCTTGATCAATGATCATCATCAAAAGCCACAGGAATGATTTGGCATCCACC 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 377 AATGAGTCTGACATCAAGGCTTGTCTAAGTCAAGCAACCTGAATTAACAGTACTT 436
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 380 AGATGAATTTGAAGTGTGAGTGTGCTAAGTTCAGTCAACCTGAATTAAGTACCAATTT 439

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QY 437 CTAATAGAACAGAAAATTTGCACTCAATAAATTTGACCTGCTCATCTATCAAGGTTACC 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 440 CTAATATACAGAAAA---TGTGACATTAATTTGACCTGCTCATCTATCAAGGTTACC 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 497 CAGAACCTAAGAGATGATTTTCAAGTCAAACTGAGAAATTCAGTACTAAGTANGATA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 497 CAGAACCTAAGAGATGATGTTTGTCTAAGAACCAAGAAATTCAGTACTAAGTANGATG 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 557 CTGTCATGAAGAAATTCCAAAATTAATGACAGAGACTGTCAACGTTTCATACAGCTGC 616
    | | | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 557 GTATTATGCAAAATTCAGAAATATGTCACAGAGCTGTACAGAGTTCATACAGCTTGT 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 617 CTTTTCAGTCCCTGAAG---CACACAATGTAGGCGCTTTTGTGCCCCGTAAGTGGAGA 673
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 617 CTGTTTCATTCCTGATGTTACGAGCAATATGACCACTCTGTATTCGGAAGCTGACA 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 674 CACTGGAGATCTGCTCTCCCTACCTTCAATATAGTGCACAACCTAAGGATTAAGACC 733
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 677 ---AGAGCGGCTTTTATCTTCACCTTTCCTATAG-----AGCTTGAGGACCTCAGC 727
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 734 CTGAACAAGGCCACTCTCCTCGATTCGGCTGTACTTGTATGTTTGTGTTTGTG 793
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 728 CTCCCCAGACACATTCCTTGGATTTACAGCTGTACTTCCACAGTTATATATGTGTA 787
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 794 GGATGTGTCTTTTAAACACTAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 853
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 788 TGTGTTTCTGTCTAATTCATGAAATGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 847
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 854 AATGTGAACCATCAAAAGGAGAGAAAGAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 913
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 848 AATGTGAACCATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 914 ACCAGTACCTGAGAGATCTGATGAAGCCCAAGTG---TATTACATTTTGAAGACAGCT 970
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 908 TCCATATACCTGAAGATGATGATGAAGCCAGCGGTGTTTAAAGTGAAGACATCTT 967
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 971 CAGCGCAAAAGATCTACATCTTT 996
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 968 CATGCAACAAAGTGAATCATGTTT 993
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RESULT 5
US-09-039-762A-33
; Sequence 33, Application US/09039762A
; Patent No. 6235073
; GENERAL INFORMATION:
; APPLICANT: Cal, Zelig
; APPLICANT: Sprent, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olsson & Hierl, Ltd.
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,762A
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OLSON, Arne M.
; REGISTRATION NUMBER: 30,203

```



```

QY      364 GTCCACAGCAACAAGAATGATTGGACCTTANAGTCGTCTACTACTCACTCAACCTGAA 423
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      490 ATTGCATTCACCACAGATGAATTTCTGAACCTGTCACTGCTTAATCTCACTCAACCTGAA 549
QY      424 ATAACAGTAGTCTTAATAGAACAGAAAATTCGGCATCATAAATTTGACCTCTCATCT 483
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      550 ATAGAACCAATTTCTAATATATACAGAAAA--TGTTGACATAAATTTGACCTGTCATCT 606
QY      484 ATACAGGTTCCCGAANAACCTAAGASATATGTTTTCAGCTAAACACTGAGAAATTTCAACT 543
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      607 ATACACGGTTAACCCAGAACCTTAACAAACATAGTGTGTTGGTAAGAACCAAGAAATTTCAACT 666
QY      544 ACTAAGTATGATCTGTCATGAGAAATTCACAAAATATGATGTGACAGAACTGTATCAACGTT 603
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Db      667 ATCGATGATGATGGTATTATGOCANAAMATCTCAGATATATGTCANAGAACTGTACGACGTT 726
QY      604 TCTATCAGCTGCCCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTCTTTTGTC 660
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      727 TCACATCAGCTTGCTGTTGTTTATTCCTCGATGTTACGAGCAATATGACCACTTCTGTATT 786
QY      661 CTGAACACTGAGACATCGAGAGATGCTGCTCCCTACCTTCATATATGATGACACACCT 720
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      787 CTGGAACACTGACA--AGACGGCGCTTTTATCTTCACCTTTCTCTATAG-----AGCTT 837
QY      721 AAGGATAAAGACCTCTGACAAAGGCGCACTTCCTGTGATTCGGGCTGTACTTGTAATGTT 780
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      838 GAGAGACCTCGACCTCCGCCACAGACACATCTCTGGATVACACTGTACTTCACACAGTT 897
QY      781 GTGTGTTTTTGTGGAGTGTGTGCTCTTAAANACTAAGAAAAGGAAAGAACGACGCT 840
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      898 ATTATATGTGTGATGATGTTTCTGTCTATTTCTATGAAATGAAAGAAAGAAAGGCGGCT 957
QY      841 GGCCCCCTCTCATGATGTGAAACCCATCAAAGGAGAGAAAGAAAGACCAACAGACAC 900
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      958 CGCAACTCTTATTAATATGTGGAACCAACACAAATGGAGAGGAGAGATGAACGACCAAG 101
QY      901 GAAGAGTACCATATCCACAGTACCTCGAAGATCTGATGAAAGCCCAGAGS---TATTACATT 957
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1018 AAAAGAGAAAAATTCACATATACCTGGAAGATCTGATGAAGCCCAAGCGGTGTTTTAAAGT 107
QY      958 TTGAAGACAGCCTCGAGCGCAAAAAGTACATACACTTTT 996
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1078 TCGAAGACATCTTCATCGACAAAAGTATACATGTTTT 1116

RESULT 2
PCT-US94-09642-1
; Sequence 1, Application PC/TUS9409642
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
; TITLE OF INVENTION: Protein and Related Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schering-plough Corporation, W-3-W
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh IIfx
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/120,606
; FILING DATE: 13-SEP-1993
; PRIOR APPLICATION DATA:

```

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: APPLICATION NUMBER: US 08/116,882
: FILING DATE: 03-SEP-1993
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Blasdale, John H. C.
: REGISTRATION NUMBER: 31,895
: REFERENCE/DOCKET NUMBER: DX0390K1
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 201-822-7398
: TELEFAX: 201-822-7039
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 1428 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: FEATURE:
:
: NAME/KEY: CDS
: LOCATION: 152..1123
:
: PCT-US94-09642-1

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Query Match	Similarity	55.5%	Score	553	DB	5	Length	1428
Best Local	Similarity	75.7%	Pred.	No.	1.3e-164			
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QY	4	GGCATTGTGACAGCAGCATATGAGGACTGATGATCACTCTCTCTGTGTGATGGCCCTCTGCTC	63					
Db	134	GGCATTGTGACAGCAGCATATGAGGACTGATGATCACTCTCTCTGTGTGATGGCCCTCTGCTC	193					
QY	64	TCTGTTGTTTCTTCATGTAAGGTCGAACCTATTTCCAAAGACCTGGAGAACTGGCAATGC	123					
Db	194	TCTGTTGTTTCTTCATGTAAGGTCGAACCTATTTCCAAAGACCTGGAGAACTGGCAATGC	253					
QY	124	CATTTTACAAACTCTCAAAACATATAGCCCTGATGAGCTGGTATTTATTTTGGCAGGACCG	183					
Db	254	CAATTTGCAAACTCTCAAAACCAAAAGCCGTGATGAGCTAGTAGTATTTTGGCAGGACCG	313					
QY	184	CATAAGCTGGTTCTCTATATGAGATATTTCAAGGCAAGGCAAAAGCCCTCAAAATGTTATCTC	243					
Db	314	GAAAATCTGGTTCTCTAAATGAGGTAATCACTTAGGCAAAAGAAATTTGACAGTGTATATTC	373					
QY	244	AAATTTAAGGGGCGCTTACAAAGCTTTTACAAAGGCAACTGGACCCTGAGATCCACAATGTT	303					
Db	374	AAGTATATGGGCGCGACAAGTTTATTTGCGACATTTGGACCCCTGAGATTCACATCTTT	433					
QY	304	CAGATCAAGGACAAAGGGGACATATCACTGTTTCACTTATTAAGGGGCCCAAGGACTA	363					
Db	434	CAGATCAAGGACAAAGGGGCTTGATCAATGATCATCCATCAACAAAAGGCCACAGAAATG	493					
QY	364	GTTCCCATGACCAAAATAGTTCATCACTATACAGTGGCTTGCTAACTTCAATGACCAACTGA	423					
Db	494	ATTCCATCTCCACCAATGAAATTTCTACCTGTGAGTGGCTTGAACTTCAAGTCAACCTGAA	553					
QY	424	ATTAAGTATACCTCTTAATATAGAACAACAAAATTCGSCATCATTAATTTGACCTGCTCATCT	483					
Db	554	ATAGTATCCAAATTTCTAATATATAACAGAAAA--TGATGTACATTAATTTGACCTGCTCATCT	610					
QY	484	ATACAGGTTTACCCAGAAACTATAGGAGATGTAATTTTCAAGCTTAACACTGAGATTTCAACT	543					
Db	611	ATACAGGTTTACCCAGAAACTATAGGAGATGTAATTTTGGCTTAAGAACCAAGATTTCAACT	670					
QY	544	ACTAGTGTGATACGTCATGAGAAATCTCAAAATTAATATGATAGCAAGCTGTACAAAGTT	603					
Db	671	ATCGAGTTATGATGATTAATATGCAAGAAATCTCAAGATTAATATGTCACAGAACTGTACAGCTT	730					
QY	604	TCTATCACTGTGCTCTTTTTCAGTCCCTCAAG---CACACAATGTAGAGGCTCTTTTGTGCC	660					
Db	731	TCTATCACTGTGCTCTTTTTCAGTCCCTCAAG---CACACAATGTAGAGGCTCTTTTGTGCT	790					
QY	661	CTGAACCTGGAGACACTGGAGATGCTGCTCTCCCTCACTTTCAATATATGATGACACAACCT	720					
Db	791	CTGAACCTGGACA---AGACGGGCGCTTTATCTTCACTCCCTCTCTATAG-----AGCTT	841					

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 ; Search time 34.5402 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-28

Perfect score: 1 atggagcatttgacagcac.....acaaagtactacatttt 996

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by the chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	55.5	1424	4	US-09-326-186B-226
2	553	55.5	1428	5	Sequence 226, App
3	540	54.2	1002	4	Sequence 1, Appl
4	540	54.2	1002	4	Sequence 33, Appl
5	540	54.2	1002	4	Sequence 33, Appl
6	540	54.2	1002	4	Sequence 33, Appl
7	540	54.2	1120	2	Sequence 11, Appl
8	540	54.2	1120	2	Sequence 1, Appl
9	540	54.2	1120	3	Sequence 1, Appl
10	540	54.2	1120	4	Sequence 22, Appl
11	540	54.2	1120	4	Sequence 22, Appl
12	540	54.2	1120	4	Sequence 22, Appl
13	540	54.2	1120	5	Sequence 3, Appl
14	540	54.2	1161	4	Sequence 22, Appl
15	540	54.2	1161	4	Sequence 24, Appl
16	540	54.2	1161	5	Sequence 24, Appl
17	535	53.7	972	4	Sequence 24, Appl
18	434.6	43.6	751	4	Sequence 11, Appl
19	434.6	43.6	751	4	Sequence 34, Appl
20	434.6	43.6	751	4	Sequence 34, Appl
21	330	33.1	1261	4	Sequence 34, Appl
22	330	33.1	1261	4	Sequence 12, Appl
23	330	33.1	1261	4	Sequence 12, Appl
24	329.6	33.1	1151	2	Sequence 3, Appl
25	329.6	33.1	1151	4	Sequence 20, Appl
26	329.6	33.1	1151	4	Sequence 20, Appl
27	329.6	33.1	1151	5	Sequence 20, Appl

28	329.6	33.1	1163	3	US-08-479-744A-22	Sequence 22, Appl
29	329.6	33.1	1163	3	US-08-280-757B-22	Sequence 22, Appl
30	225	22.6	330	3	US-08-479-744A-44	Sequence 44, Appl
31	225	22.6	330	3	US-08-280-757B-44	Sequence 44, Appl
32	159	16.0	306	3	US-08-479-744A-46	Sequence 46, Appl
33	159	16.0	306	3	US-08-280-757B-46	Sequence 46, Appl
34	101.8	10.2	210	4	US-08-205-697A-31	Sequence 31, Appl
35	101.8	10.2	210	4	US-08-702-525-31	Sequence 31, Appl
36	101.8	10.2	210	5	PCT-US95-02576-31	Sequence 41, Appl
37	59.6	6.0	195	4	US-08-205-697A-41	Sequence 41, Appl
38	59.6	6.0	195	4	US-08-702-525-41	Sequence 41, Appl
39	59.6	6.0	195	5	PCT-US95-02576-41	Sequence 41, Appl
40	37.2	3.7	7218	1	US-08-232-463-14	Sequence 14, Appl
41	33.8	3.4	2160	2	US-08-840-236-5	Sequence 2, Appl
42	33.8	3.4	2160	2	US-08-840-236-5	Sequence 5, Appl
43	33.8	3.4	2160	2	US-08-505-448A-2	Sequence 2, Appl
44	33.8	3.4	2160	2	US-08-505-448A-5	Sequence 5, Appl
45	33.6	3.4	492	4	US-09-328-111-335	Sequence 335, Appl

ALIGNMENTS

RESULT 1
US-09-326-186B-226
; Sequence 226, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326.186B
; PRIOR APPLICATION NUMBER: 1999-06-04
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-326-186B-226

Query Match 55.5%; Score 553; DB 4; Length 1424;

Best Local Similarity 75.7%; Pred. No. 1.3e-164; Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY	4	GGCATTGTGACAGCTATGGGACTGAGTCACACTCTCTTGATGGCCCTGCTC	63
DB	130	GGCATTGTGACAGCTATGGGACTGAGTCACACTCTCTTGATGGCCCTGCTC	189
QY	64	TCTGTGTTTTCATGAGAGTCAAGCATATTTCAACAAAGAGTGGAGTGCATTC	123
DB	190	TCTGTGTTTTCATGAGAGTCAAGCATATTTCAACAAAGAGTGGAGTGCATTC	249
QY	124	CATTTCACAACTCTCAAAACATAGAGCTGAGTGTAGTATTTGGACGAGCAG	183
DB	250	CAATTTCACAACTCTCAAAACATAGAGCTGAGTGTAGTATTTGGACGAGCAG	309
QY	184	GATAAGCTGGTCTGTGATATTCAGAGCGCAAGAAAGCAACCTCAAAATGTCATC	243
DB	310	GATAAGCTGGTCTGTGATATTCAGAGCGCAAGAAAGCAACCTCAAAATGTCATC	369
QY	244	AAATTAAGGCGCTTGAAGCTTGAACAAGCAAGCAAGCCGAGACCTCAATGTT	303
DB	370	AAATTAAGGCGCTTGAAGCTTGAACAAGCAAGCAAGCCGAGACCTCAATGTT	429
QY	304	CAGATCAAGCAAGGCGCATATCACTGTTTCATTATTAAGGCGCAAGGAGCTA	363
DB	430	CAGATCAAGCAAGGCGCTTGTATCATATCATCATCAACAAAGCCGACAGGATG	489

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Db 1236 CTGTCATGAGAAATCTCAAAATATATGTACACAGACTTACAAAGTTTCTATCAGCTTGT 1177
QY 617 CTTTTCAGTCCCTGAAGCACACATGTGAGCGCTTTTGTGCCCTGAAACTGGAGACAC 676
Db 1176 CCTTCATGATCCCTGAAGCAGCATGTGAGCATTTCTGTGTGCTGCAACTTGAGTCAA 1117
QY 677 TGGAGATGCTGCTCTGCTTACCTTTCATATATGATGACACACCTTAGSATTAAGA 731
Db 1116 T---GAAGCTTCCCTCCTTACCTTATATATATGAAACAAACAAGTGAAGAGAA 1065
```

Search completed: October 19, 2002, 23:33:20
Job time : 157.774 secs

CC diagnosis and drug screening.

XX Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;

Query Match 58.5%; Score 582.2; DB 20; Length 1795;

Best Local Similarity 89.4%; Pred. No. 6e-159;

Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

```
OY 17 GCACATGAGGAGTACACCTCTCTGTATGGCCCTCTGCTCTGTGTTCTT 76
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 GCACATGAGGAGTACACCTCTCTGTATGGCCCTCTGCTCTGTGTTCTT 79
OY 77 CCATGAGAGTCAAGCATATTTCAACAGACTGGAGACTGCCATGTTTACAACT 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 CCATGAGAGTCAAGCATATTTCAACAGACTGGAGACTGCCATGTTTACAACT 139
OY 137 CTCAAACATTAAGCCGATGAGCTGTATTTTGGAGAGCAGATTAAGCTGTTT 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 CTCAAACATTAAGCCGATGAGCTGTATTTTGGAGAGCAGATTAAGCTGTTT 199
OY 197 TGTATGATATTCAGAGGCAAGAACCCCTCAAAATGTTTCATCTCAAAATTAAGGCC 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 TGTACAGACTATACAGAGCAAGAACCCCTCAAAATGTTTCATCTCAAAATTAAGGCC 259
OY 257 GTACAAAGCTTTGACAAAGCAACTGGACCTGAGACTCCACATGTTTCAAGTCAAGACA 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 260 GCACAAAGCTTTGACAAAGCAACTGGACCTGAGACTCCATATATGAGATCAAGAGACA 319
OY 317 AGGCAACATATCAGCTGTTTCATTTAAGAGGCCCAAGAGACTAGTCCCATGACAC 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 320 AGGCTGTATATATGTTTCTGTTTCATTAAGAGGCCCAAGAGACTAGTCCCATGACAC 379
OY 377 AATGAGTCTGACCTATTCAGTGTGTTGCTTAAGTCAAGCTGAATAACAGTAACTT 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 380 AATGAGTCTGACCTATTCAGTGTGTTGCTTAAGTCAAGCTGAATAACAGTAACTT 439
OY 437 CTATATGAAGCAAAATTTGTCATCAATTAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAG 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 440 CTATATGAAGCAAAATTTGTCATCAATTAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAG 499
OY 497 CAGAACCTTAAGGAGATGATTTTTCAGTCAAACTGAGAGATTTCACTAAGTATGATA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 500 CAGAACCTTAAGGAGATGATTTTTCAGTCAAACTGAGAGATTTCACTAAGTATGATA 559
OY 557 CTGTATGAAGAAATCTCAAAATATGAGACGAAGCTGTAAGCTTTCTACAGCTTGC 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 560 CTGTATGAAGAAATCTCAAAATATGAGACGAAGCTGTAAGCTTTCTACAGCTTGT 619
OY 617 CTTTTCAGTCCCTGAGACACATGAGAGGCTTTTGGCCCTGAACCTGGAGACAC 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 620 CTTTTCAGTCCCTGAGACACATGAGAGGCTTTTGGCCCTGAACCTGGAGACAC 679
OY 677 TGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGACAAACCTAAGATTAAGA 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 680 T---GAGAGCTTCCCTCTACCTTATATATGAAGAACCAAGAGTGAAGAGAA 731
```

RESULT 15

AA227922/c

ID AA227922 standard; DNA; 1795 BP.

AA227922;

20-DEC-1999 (first entry)

XX Canine B7-2s gene complementary DNA sequence.

XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; canine;

XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

```
PN W09947558-A2.
XX 23-SEP-1999.
XX 19-MAR-1999; 99WO-US06187.
XX 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX (HESK-) HESKA CORP.
XX Slim G, Yang S, Sellins KS;
PI WPI; 1999-571822/48.
DR New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
PS Claim 1; Page 112-114; 148pp; English.
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;
OY 17 GCACATGAGGAGTACACCTCTCTGTATGGCCCTCTGCTCTGTGTTCTT 76
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1776 GCACATGAGGAGTACACCTCTCTGTATGGCCCTCTGCTCTGTGTTCTT 1717
OY 77 CCATGAGAGTCAAGCATATTTCAACAGACTGGAGACTGCCATGTTTACAAACT 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1716 CCATGAGAGTCAAGCATATTTCAACAGACTGGAGACTGCCATGTTTACAAACT 1657
OY 137 CTCAAAACATTAAGCCTGAGTACCTGTTATTTGGCAGGACCAAGATTAAGCTGTTT 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1656 CTCAAAACATTAAGCCTGAGTACCTGTTATTTGGCAGGACCAAGATTAAGCTGTTT 1597
OY 197 TGTATGATATTCAGAGGCAAGGACCTCAAAATGTTTCATCTCAATATTAAGGCC 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1596 TGTATGATATTCAGAGGCAAGGACCTCAAAATGTTTCATCTCAATATTAAGGCC 1537
OY 257 GTCAACACTTTGACAAAGCAAGCAAGTGAAGCTCCCATGTTTCAAGATTAAGGACA 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1536 GTCAACACTTTGACAAAGCAAGTGAAGCTCCCATGTTTCAAGATTAAGGACA 1477
OY 317 AGGCAACATATCAGCTGTTTCATTTAATTAAGAGGCCCAAGAGACTAGTTCATGACAC 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1476 AGGCTGTATCAATGTTTCTGTTTCATTAATTAAGAGGCCCAAGAGACTAGTTCATGACAC 1417
OY 377 AATGAGTCTGACCTATTCAGTGTGTTGCTTAAGTCAAGTGAATTAAGAGTAACTT 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1416 AATGAGTCTGACCTATTCAGTGTGTTGCTTAAGTCAAGTGAATTAAGAGTAACTT 1357
OY 437 CTATATGAAGCAAAATTTGCGCATATTAATTAAGTCAAGTGAATTAAGAGTAACTT 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1356 CTATATGAAGCAAAATTTGCGCATATTAATTAAGTCAAGTGAATTAAGAGTAACTT 1297
OY 497 CAGAACCTTAAGGAGATGATTTTTCAGCTTAAGCAAGTGAATTAAGTGAATTAAGTGA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1296 CAGAACCTTAAGGAGATGATTTTTCAGCTTAAGCAAGTGAATTAAGTGAATTAAGTGA 1237
OY 557 CTGTATGAAGAAATCTCAAAATATGAGACGAAGACTGTACAAAGCTTTCTATACCTTGC 616
```


RESULT 13
AAZ27924/C
ID AAZ27924 standard; DNA; 840 BP.
XX
AC AAZ27924;
XX
DT 20-DEC-1999 (first entry)
XX
DE Complementary strand of canine B7-2S coding sequence.
XX
KM B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 115; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;

Query Match 58.5%; Score 582.2; DB 20; Length 840;
Best Local Similarity 89.4%; Pred. No. 4; 2e-159;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 17 GCACATATGGAGTACACTCTCTGTGATGGCCCTCGCTGCTGCTGCTT 76
DB 827 GCACTATGCACTGATTAACATTTCTTTGTGATGACCTCTGCTTAATGCTGCTT 768
QY 77 CCATGAGAGTCAAGCATATTTCAACAGACTGAGAACTGCATGCCATTTTACAACT 136
DB 767 CCATGAGAGTCAAGCATATTTCAACAGACTGAGAACTGCATGCCATTTTACAACT 708
QY 137 CTCAAAACATAGCCCTGAGTGTAGTATTTTGGCAGACAGATTAAGCTGCTTC 196
DB 707 CTCAAAACATAGCCCTGAGTGTAGTATTTTGGCAGACAGATTAAGCTGCTGCTTC 648
QY 197 TGTATGAGATATTCAGAGCAAGAACCCCTCAAAATTTTCATGCTCAATATTAAGGCC 256
DB 647 TGTACGAGCTATACAGAGCAAGAACCCCTCAAAATTTTCATGCTCAATATTAAGGCC 588
QY 257 GTACAAAGCTTTGACAGAGCAAGCAAGCCCTGAGACTCCACATGTTTGCATCAAGGACA 316
DB 587 GTCACAGCTTTGACAGAGCAAGCAAGCCCTGAGACTCCACATGTTTGCATCAAGGACA 528
QY 317 AGGGACATATCTACTGTTTCAATTAATAAGGCCCAAGAGACTAGTCCCATGACCC 376

DB 527 AGGGCTTGTATCAATGTTTCCTTCATCAATAAGGCCCAAGAGACTGTTCCATGACCC 468
QY 377 AATGAGTTCGACCTATCAAGTCTGTGCTAATCTCACTCAACCGAATATAGTACTT 436
DB 467 AGATGAATTTCTGACCTATCAAGTCTGTGCTAATCTCACTCAACCGAATATAGTACTT 408
QY 437 CTAATAGAACAGAAATTTCTGACATCAATAATTTGACCTGCTCATCTATCAAGGTACC 496
DB 407 CTAATAGAACAGAAATTTCTGACATCAATAATTTGACCTGCTCATCTATCAAGGTACC 348
QY 497 CAGAACCTAAGAGATGATTTTCACTCAAGCACTGCAATTTCACTCACTCACTGATATA 556
DB 347 CAGAACCCAGAGATGATTTTGGTAAACCGGAATTCAGTCAAGTATGATA 288
QY 557 CTGTCATGAGAAATTCATAAATATGAGACAACTGCAACGTTTCTATCAGCTTGC 616
DB 287 CTGTCATGAGAAATTCATAAATATGAGACAACTGCAACGTTTCTATCAGCTTGT 228
QY 617 CTTTTCAGTCCCTGAGACACAAATGTAGCGCTTTTGTGCCCCGTAACCTGAGACAC 676
DB 227 CTTTCTCAGTCCCTGAGACCAATGTAGCGATCTTCTGTCTCCTCAACTGATGCAA 168
QY 677 TGGAGATCTGCTCTCCCTACCTTCAATATAGATGACCAACCTAAGGATTAAGA 731
DB 167 T--GAAGCTTCCTCCCTACCTTATATATGAACCAACAAAGTGGAGAGAAA 116

RESULT 14
AAZ27921
ID AAZ27921 standard; DNA; 1795 BP.
XX
AC AAZ27921;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein encoding DNA.
XX
KM B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
DR P-PSDB; AAY41078.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 109-111; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,

```
Db 394 TAGAGTCTGACCTATCAGAGCTTGCTTAACCTGACACCTGAACCTGAACCTACTACTACTA 453
Qy 440 ATAGAACAGAAATTTGTCATCATTAATTTGACCTGCTATCTATACAGGTTCCAG 499
Db 454 ATCACACAGAAATTTCTG---TCATTAATTTTACCTGCTCTACTCTACACAGAGTACCCAG 510
Qy 500 AACCTAAGAGATGATTTTTCAGCTAATACCTGAGAAATTCACCTACTAATGATGATG 559
Db 511 AACCCAGAGATGATATATGTTGTAATATACAGAAATTCACCTGAGCATGATGCTG 570
Qy 560 TCATGAGAAATTTCTCAAAATATATGACAGAACCTGACACCTTTCTATGACCTTGCTT 619
Db 571 ACATGAGAAATTTCTCAAAATATATGACAGAACCTGACACCTTTCTATGACCTTGCTT 630
Qy 620 TTTCAAGTCCCTGACAGACACATGAGAGCTTTTGTGCCCTGAACCTGGAGACACTGG 679
Db 631 TTCCCATCTCCCTCCGAGACAAATGTGAGCATGCTGTGTCTGCAACTTGAGCCAGCA 690
Qy 680 AGA---TGCTGCTCTCCCTACCTTTCAATATATGATGACACACCTAAGGATAAAGACCTG 736
Db 691 AGACACATGCTTTTCTCCCTACCTTTGAATATATGATGCAAGGACACCTGAGCAACCCCTG 750
Qy 737 AACAGGACCATCTCTCTGATGATGCGGCTGTACTTGTATGTTTGTGTTTGTGGA 796
Db 751 TCCACAGACACATCTCTGATGATGAGCTCTACTGTAACTGTGCTGTGTGTGGA 810
Qy 797 TGGTGTCTTTTAAACACTAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
Db 811 TGGTGTCTTTTAAACACTAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
Qy 857 ---GTGAAACATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 913
Db 871 GTGGAGAAACATCAAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926
Qy 914 ACCAGTACCTGAGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
Db 927 ---GAAGTCATTAACGATCTGATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 984
Qy 971 CAGGCGACAAAAGTACTACACATTTT 996
Db 985 CAGATGACAAACGACTACTACAGATTTT 1010

RESULT 12
AAZ27923
ID AAZ27923 standard; DNA; 840 BP.
XX
AC AAZ27923;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein coding sequence.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN MO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
```

```
DR WPI: 1999-571822/48.
DR P-PSDB: AAY41078.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
PS Claim 1; Page 114; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP; 278 A; 181 C; 167 G; 214 T; 0 other;
XX
Query Match 58.5%; Score 582.2; DB 20; Length 840;
Best Local Similarity 89.4%; Pred. No 4.2e-159;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

Qy 17 GCATATGAGAGTGAATCAACATCTCTTGTGATGAGCCCTGCTCTGCTGTGTTCTT 76
Db 14 GCATATGAGAGTGAATCAACATCTCTTGTGATGAGCCCTGCTCTGCTGTGTTCTT 73
Qy 77 CCATGAGAGTGAATCAACATCTCTTGTGATGAGCCCTGCTCTGCTGTGTTCTT 136
Db 74 CCATGAGAGTGAATCAACATCTCTTGTGATGAGCCCTGCTCTGCTGTGTTCTT 133
Qy 137 CTCAAACATTAAGCTGATGAGCTGTGATGAGCCCTGCTCTGCTGTGTTCTT 196
Db 134 CTCAAACATTAAGCTGATGAGCTGTGATGAGCCCTGCTCTGCTGTGTTCTT 193
Qy 197 TGTATGATATTCAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256
Db 194 TGTATGATATTCAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 253
Qy 257 GTACAGCTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
Db 254 GCACAGCTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 313
Qy 317 AGGCGACATATCACTGTTTCATTTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 376
Db 314 AGGCGCTGTATCAATGTTTGTTCATATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 373
Qy 377 AATGAGTTTGAACATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
Db 374 AGATGAATTCAGACATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
Qy 437 CTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
Db 434 CTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 493
Qy 497 CAGAACCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 556
Db 494 CAGAACCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 553
Qy 557 CTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 616
Db 554 CTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 613
Qy 617 CTTTTCAGTCCCTGAAGGACACATGAGAGCTCTTTTGTGCCCTGAAAGCTGAGAGAC 676
Db 614 CTTTTCAGTCCCTGAAGGACACATGAGAGCTCTTTTGTGCCCTGAAAGCTGAGAGAC 673
Qy 677 TGGAGATGCTGCTCTCACTTTCAATATGATGAGAGAGAGAGAGAGAGAGAGAGAG 731
Db 674 T---GAAGCTTCCCTCCCTCACTTTATATATGAGAGAGAGAGAGAGAGAGAGAGAG 725
```


CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX
SQ Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;

Query Match 78.8%; Score 784.8; DB 20; Length 1897;

Best Local Similarity 89.0%; Pred. No. 7.1e-218;

Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

```
QY 17 GCACATATGGAGTACAGTACACTCTCTCTGGATGGCCCTCTGCTCTCTGTTTCTT 76
DB 19 GCACATATGGAGTACAGTACACTCTCTCTGGATGGCCCTCTGCTCTCTGTTTCTT 78
QY 77 CCATGAAGAGTCAACATATTTCAACAGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 136
DB 79 CCATGAAGAGTCAACATATTTCAACAGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 138
QY 137 CTCAAAACATTAAGCTGGATGAGTGTATATTTTGGCAGACAGATAGCTGTTTC 196
DB 139 CTCAAAACATTAAGCTGGATGAGTGTATATTTTGGCAGACAGATAGCTGTTTC 198
QY 197 TGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCATCTCAATATAAGGCC 256
DB 199 TGTACGAGCTATACAGAGCAAGAGAACCTCAAAATGTTTCATCTCAATATAAGGCC 258
QY 257 GTACAAAGCTTTGACAAAGCAACTGACCCCTGAGACCTCCAAATGTTTCATCTCAAGGACA 316
DB 259 GCACAAAGCTTTGACAAAGCAACTTGGACCCCTGAGACCTCCAAATATTTTCAAGGACA 318
QY 317 AGGGCAATATTCATCTGTTTCATTTATTAAGGCCCAAGAGTACTTCCATGCAACC 376
DB 319 AGGGCTTATATCAATGTTTCGTTTCATTTATTAAGGCCCAAGAGTACTTCCATGCAACC 378
QY 377 AATGAGTCTGACCTATACAGTCTGCTGCTTACCTTACGCAACCTGAAATACAGTACTT 436
DB 379 AGATGAATCTGACCTATACAGTCTGCTGCTTACCTTACGCAACCTGAAATATTTGTAACCT 438
QY 437 CTAAATGAGACAGAAATTTCTGGCATCATAAATTTGACCTGCTCATCTTACAGGTTTACC 496
DB 439 CTAAATGAGACAGAAATTTCTGGCATCATAAATTTGACCTGCTCATCTTACAGGTTTACC 498
QY 497 CAGAACTTAAGAGATGATTTTTCAGCTAAACCTGAGAAATTCATCTAATAGATGATA 556
DB 499 CAGAACTTAAGAGATGATTTTTCAGCTAAACCTGAGAAATTCATCTAATAGATGATA 558
QY 557 CTGATGAGAGAAATCTCAAAATATATGACAGAACTGTACAGCTTCTTCAAGCTTGC 616
DB 559 CTGATGAGAGAAATCTCAAAATATATGACAGAACTGTACAGCTTCTTCAAGCTTGC 618
QY 617 CTCTTTTCAAGCTGACAGACACATGTGAGCTCTTTTGGCCCTGAACTGAGAGAC 676
DB 619 CTTTCTCAGTCCCTGACAGACAGCAATGTGAGCAATCTTCTGCTCTGCAACTGTAGTCAA 678
QY 677 TGGAGATGCTGCTCTCCCTACCTTCAATATATGACCAACCTTAAGATTAAGACCTTG 736
DB 679 T---GAACCTTCCCTTACCTATATATATATGATGACA---TAGCAAAACCCACCCTG 732
QY 737 AACAAGGCCACTTCTCTGAGATTTGGGCTGTACTTGTATATTTTGTGTTTGTGGGA 796
DB 739 ATGGAGACCATATCTCTGAGATTTGGGCTGTGATATTTGATTTTGTGTTGTTGTTGGA 792
QY 797 TGTGTCTCTTTAAACATAAGAAAGAGAGAGAGACAGACCTGGGCCCTCTCATGAT 856
DB 799 TGTGTCTCTTTCTTCAACATAAGAAAGAGAGAGAGACAGACCTGGGCCCTCTCATGAT 852
QY 857 GTGAAACCATCAAAAGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGATACATACC 916
DB 859 GTGAAACCATCAAAAGGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGATACATACC 912
QY 917 ACATGACCTGAGAGATCTGATTAAGCCCAAGTATTTAATTTTGAACAGAGCTCAGGCC 976
DB 919 ACATGACCTGAGAGATCTGATTAAGCCCAAGTATTTAATTTTGAACAGAGCTCAGGCC 978
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DB 913 ATGAAGAGAGAGATCTGATGAAGCCCAAGTGTGTATACATTTGCAAGACAGCTTACGCC 972
QY 977 ACAAGAGTACTACATTTT 996
DB 973 ACACAGTACTACAGCTTT 992
```

RESULT 10
AAZ27914/C
ID AAZ27914 standard; DNA; 1897 BP.
XX
AC AAZ27914;
XX
XX 20-DBC-1999 (first entry)
XX
DE Canine B7-2 gene complementary DNA sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
OS Canis familiaris.
XX
PN W09947558-A2.
XX
PD 23-SEP-1999.
XX
PE 19-MAR-1999; 99MO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G. Yang S. Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating; e.g. autoimmune and atopic diseases -
XX
XX
PS Claim 1; Page 101-102; 148pp; English.

XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SQ Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;

Query Match 78.8%; Score 784.8; DB 20; Length 1897;

Best Local Similarity 89.0%; Pred. No. 7.1e-218;

Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

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QY 17 GCACATATGGAGTACAGTACACTCTCTCTGGATGGCCCTCTGCTCTCTGTTTCTT 76
DB 1879 GCACATATGGAGTACAGTACACTCTCTCTGGATGGCCCTCTGCTCTCTGTTTCTT 1820
QY 77 CCATGAAGAGTCAACATATTTCAACAGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 136
DB 1819 CCATGAAGAGTCAACATATTTCAACAGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1760
QY 137 CTCAAAACATTAAGCTGGATGAGTGTATATTTTGGCAGACAGATAGCTGTTTC 196
DB 1759 CTCAAAACATTAAGCTGGATGAGTGTATATTTTGGCAGACAGATAGCTGTTTC 1700
QY 197 TGTATGAGATATTCAGAGGCAAGAGAGAACCTCAAAATGTTTCATCTCAATATAAGGCC 256
DB 199 TGTATGAGATATTCAGAGGCAAGAGAGAACCTCAAAATGTTTCATCTCAATATAAGGCC 258
```

XX 23-SEP-1999.
 PD
 XX 19-MAR-1999; 99WO-US06187.
 PF
 XX 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 PI Sim G, Yang S, Sellins KS;
 XX
 DR WPI: 1999-571822/48.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 XX treating, e.g. autoimmune and atopic diseases -
 PS Claim 1: Page 103-104; 148pp; English.
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Query Match 78.8%; Score 784.8; DB 20; Length 987;
 Best local Similarity 89.0%; Pred. No. 5.2e-218;
 Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 17 GCACATATGGACGAGTACACCTCTCTGTGATGGCCCTCTGCTCTGTGTTCTT 76
 DB 974 GCACATATGGACGAGTAAACCTCTTGTGTGATGACCTCTGCTCTGTGTTCTT 915
 QY 77 CCATGAAGAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGCCATTTTACAAC 136
 DB 914 CCATGAAGAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGCCATTTTACAAC 855
 QY 137 CTCAAAACATTAAGCTGGATGAGCTGTATTTTGGAGACACGATTAAGCTGTTC 196
 DB 854 CTCAAAACATTAAGCTGGATGAGCTGTATTTTGGAGACACGATTAAGCTGTTC 795
 QY 197 TGTATGAGATATTCAGAGCAAGAGAACCTCAAAATGTTCATCAATATTAAGGGCC 256
 DB 794 TGTACGAGCTATACAGAGGCAAGAGAACCTCAAAATGTTCATCAATATTAAGGGCC 735
 QY 257 GTACAAAGCTTTGACAAGAGCACTGGACCTGGACTCCACATATTTAGATTAAGAGAA 316
 DB 734 GCACAAGCTTTGACAAGAGCAATTTGGACCTGGACTCCATATATTTAGATTAAGAGAA 675
 QY 317 AGGGACATATCACTGTTTCATTCATTAAGAGGCCCAAGAGCTAGTCCCATCCACC 376
 DB 674 AGGGCTGTATCAATGTTTCATTCATTAAGAGGCCCAAGAGCTAGTCCCATCCACC 615
 QY 377 AAATGAGTCTGACCTATGCTGTGCTAAGTCACTGTAAGCTGAATTAAGCTAAGT 436
 DB 614 AGATGAATTTGACCTATGCTGTGCTAAGTCACTGTAAGCTGAATTAAGCTAAGT 555
 QY 437 CTATAGAACAAGAAATTTGCGATCATTAATTTGACCTGCTCATTAATCAAGGTTTACC 496
 DB 554 CTATAGAACAAGAAATTTGCGATCATTAATTTGACCTGCTCATTAATCAAGGTTTACC 495
 QY 497 CAGAACCTTAAGAGATTAATTTAGCTAAACCTGAGAAATTAAGTAACTAGTAAATGA 556
 DB 494 CAGAACCTTAAGAGATTAATTTAGCTAAACCTGAGAAATTAAGTAACTAGTAAATGA 435
 QY 557 CTGTCAAGAGAAATCTCAAAATTAATGTGACAGAACTGTAACGTTTCATAGCTTGC 616
 DB 557 CTGTCAAGAGAAATCTCAAAATTAATGTGACAGAACTGTAACGTTTCATAGCTTGC 616

DB 434 CTGTCAAGAGAAATCTCAAAATTAATGTGACAGAACTGTAACAACTTTTCATGAGCTTGT 375
 QY 617 CTTTTAGTCCCTGAGAGCAACATGTGAGCGCTTTTGTGCGCTGAACCTGAGAGAC 676
 DB 374 CTTTCTAGTCCCTGAGAGCAACATGTGAGCATCTTTGTGTCTGCAACTGAGTCA 315
 QY 677 TGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
 DB 314 T---GAAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
 QY 737 AACAAAGCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
 DB 260 ATGGAGACCATCTCTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
 QY 797 TGGTGTCTTTAAACCTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 856
 DB 200 TGGTGTCTTTCTAAGCACTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 141
 QY 857 GTGAAACCATCAAAAGGAGAGAAAGAGCAAAAGACCAAGCAAGAAAGATACCATACC 916
 DB 140 GTGAAACCAAAAGTGGAGAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 81
 QY 917 ACGTACCTGAGAGATCTGATGAAGCCAGTGTATTAATTTTGAAGACAGAGCTGAGGGC 976
 DB 80 ATGAAACGGAAGATCTGATGAAGCCAGTGTGTTAATTTTGAAGACAGCTTGAAGGGC 21
 QY 977 ACAAAAGTACTACATTTT 996
 DB 20 ACAACGATCTACACAGTTT 1

RESULT 9
 AA227913
 ID AA227913 standard; DNA; 1897 BP.

XX AA227913;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Canine B7-2 protein encoding DNA.
 XX
 KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; canine;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06187.
 XX
 PR 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Sellins KS;
 XX
 DR WPI: 1999-571822/48.
 DR P-PSDB; AAIV41076.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 XX treating, e.g. autoimmune and atopic diseases -
 PS Claim 1: Page 97-99; 148pp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

|||||
DB 1023 AAGACAGCCTCAGGAGGACAAAAAT 1046
RESULT 6
AA234785
ID AA234785 standard; cDNA: 1080 BP.
AC AA234785;
XX
DT 15-FEB-2000 (first entry)
XX
DE Cat CD86 (B7-2) cDNA.
XX
KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
KM FIV; feline leukaemia virus; feline infectious peritonitis virus;
KM feline panleukopenia virus; feline calicivirus; feline reovirus-3;
KM feline rotavirus; feline coronavirus; feline syncytial virus;
KM feline sarcoma virus; feline herpesvirus; feline Borna disease;
KM rabies virus; chlamydia; toxoplasmosis gondii; dirofilaria immitis;
KM parasite; autoimmune disease; transplant rejection; therapy; ss.
XX
OS Felis domesticus.
XX
FH Key Location/Qualifiers
FT CDS 63..1055
FT CDS /*tag= a
XX
PN WO957271-A2.
XX
PD 11-NOV-1999.
XX
PE 30-APR-1999; 99WO-US09502.
XX
PR 01-MAY-1998; 98US-0071699.
XX
PA (TEXAS) TEXAS A & M SYSTEM.
XX
PI Collison EW, Hash SM, Choi I;
XX
DR WPI: 2000-052972/04.
DR P-PSDB: AAY32278.
XX
PT Novel feline proteins used to produce feline vaccines which prevent
PT infectious disease or to promote growth in homologous or heterologous
PT species -
XX
PS Claim 6; Fig 3A; 186bp; English.
XX
CC This is the nucleotide sequence of cDNA encoding feline CD86
CC (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
CC peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
CC comprising nucleic acid encoding feline CD86 ligand or feline
CC soluble CD86 ligand is designated PST-2#19-2/011298 (ATCC 209821).
CC The coexpression of CD86 with the costimulatory molecules CD28 (see
CC AAY32279) and a tumour antigen or an antigen from a pathogenic
CC organism has the ability to activate or enhance activation of
CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
CC the ability to regulate activation of T-lymphocytes. The invention
CC provides isolated nucleic acids encoding feline CD86 ligand.
CC feline CD86 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
CC (CD152) receptor, as well as vectors comprising the nucleic acids,
CC and polypeptides encoded by the nucleic acids. It also provides
CC vaccines comprising the CD86, CD86, CD28 or CTLA-4 polypeptides and
CC further comprising immunogens derived from pathogens, especially
CC feline immunodeficiency virus (FIV), feline leukaemia virus,
CC feline infectious peritonitis virus, feline panleukopenia virus,
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
CC herpesvirus, feline Borna disease virus, rabies virus, chlamydia,
CC toxoplasmosis gondii, dirofilaria immitis, or a flea, bacterial
CC pathogen, or parasite (all claimed). Vaccines capable of
CC enhancing an immune response, and vaccines capable of suppressing

CC an immune response (suitable for treating an autoimmune disease
CC or tissue or organ transplant rejection) are claimed. The
CC nucleic acids may be used for gene therapy or antisense therapy
CC protocols.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
Query Match 98.3%; Score 979.2; DB 21; Length 1080;
Best Local Similarity 99.7%; Pred. No. 1.5e-274;
Matches 981; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCATTTTGTGACAGCACTATGGAGCAGACACACTCTCTGTGATGGCCCTCCG 60
DB 63 ATGGCATTTTGTGACAGCACTATGGAGCAGACACTCTCTGTGATGGCCCTCTG 122
QY 61 CTCCTGTGTTTCTTCCATGAAGAGTCAAGCATATTTTACAAAGACTGAGAACTGCCA 120
DB 123 CTCTCTGTGTTTCTTCCATGAAGAGTCAAGCATATTTTACAAAGACTGAGAACTGCCA 182
QY 121 TGGCAATTTTACAAACTCTCAAAACATTAAGCTGGATGAGCTGTAGTATTTTGGCAGAC 180
DB 183 TGGCAATTTTACAAACTCTCAAAACATTAAGCTGGATGAGCTGTAGTATTTTGGCAGAC 242
QY 181 CAGGATAGCTGTTCTGTATGATATTCAGATTCAGAGCAAGAGAACCTCAAAATGTTTCA 240
DB 243 CAGGATAGCTGTTCTGTATGATATTCAGAGCAAGAGAACCTCAAAATGTTTCA 302
QY 241 CTCNAATATTAAGGCGCTGTACAGCTTTTGACAAAGACACTGACCCCTGAGACTCCCAAT 300
DB 303 CTCNAATATTAAGGCGCTGTACAGCTTTTGACAAAGACACTGACCCCTGAGACTCCCAAT 362
QY 301 GTTCAGATCAAGGACAAAGGCGACATATCACTGTTTCAATTCATTTATAAGGCCCAAGGA 360
DB 363 GTTCAGATCAAGGACAAAGGCGACATATCACTGTTTCAATTCATTTATAAGGCCCAAGGA 422
QY 361 CTAGTCCCAAGCAACCAATGAGTTGACCTATCAAGTGGCTGCTTAAGTCAAGTCAACCT 420
DB 423 CTAGTCCCAAGCAACCAATGAGTTGACCTATCAAGTGGCTGCTTAAGTCAAGTCAACCT 482
QY 421 GAATTAACAGTAACCTTCTAATAGAACAGAAATTTGGCATCATAAATTTGACCTGCTCA 480
DB 483 GAATTAACAGTAACCTTCTAATAGAACAGAAATTTGGCATCATAAATTTGACCTGCTCA 542
QY 481 TCTATACAGATTATCCAGAACCACTAAGAGATGATTTTACGTAAACCTGAGAAATTCGA 540
DB 543 TCTATACAGATTATCCAGAACCACTAAGAGATGATTTTACGTAAACCTGAGAAATTCGA 602
QY 541 ACTACTAAGTATGATGATCTGATCATGAAGAAATCTCAAAATATATGATGACAGAACTGTACAAC 600
DB 603 ACTACTAAGTATGATGATCTGATCATGAAGAAATCTCAAAATATATGATGACAGAACTGTACAAC 662
QY 601 GTTTCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCC 660
DB 663 GTTTCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCC 722
QY 661 CTGAAATCGAGACACTGAGAGATGCTGCTCTCCCTACCTTCAATATATGATGACAAACCT 720
DB 723 CTGAAATCGAGACACTGAGAGATGCTGCTCTCCCTACCTTCAATATATGATGACAAACCT 782
QY 721 AAGATATAAGACCTGTGAACAAGGCACTCTGTGATTCGGCTGTACTTGTATGTATT 780
DB 783 AAGATATAAGACCTGTGAACAAGGCACTCTGTGATTCGGCTGTACTTGTATGTATT 842
QY 781 GTTGTATTTTGTGGAGTGTCTCTTTAAACACTAAGGAAAGAAAGAAAGCAAGCGCT 840
DB 843 GTTGTATTTTGTGGAGTGTCTCTTTAAACACTAAGGAAAGAAAGCAAGCGCT 902
QY 841 GGCCCTCTCTGATGATGAAATGAAACCATCAAAAGGAGAAAGAGCAACAGACCAAC 900
DB 903 GGCCCTCTCTGATGATGAAATGAAACCATCAAAAGGAGAAAGAGCAACAGACCAAC 962
QY 901 GAAAGATGACCATTCACATGATCTGAGAGATTCGATGAGCCCAAGTGTATTAACATTTTG 960

|||||
Db 1872 GTGTGTTTTGTGGAGTGTCTCTTTAAACACTAAGGAAAGGAAAGACAGCCT 1813
QY 841 GGCCCCCTCTCTGATGATGGAACCATCAAAAGGAGAGAAAGAGCAACAGACCAAC 900
Db 1812 GGCCCCCTCTCTGATGATGGAACCATCAAAAGGAGAGAAAGAGCAACAGACCAAC 1753
QY 901 GAAAGAGTACCATACCAAGTACTGAGATCTGATGATGAGCCCAAGTATTAACATTG 960
Db 1752 GAAAGAGTACCATACCAAGTACTGAGATCTGATGATGAGCCCAAGTATTAACATTG 1693
QY 961 AAGACAGCTTCAGGCGACAAAGTACTACATTTT 996
Db 1692 AAGACAGCTTCAGGCGACAAAGTACTACATTTT 1657

RESULT 5
AAZ34838
ID AAZ34838 standard; cDNA; 1080 BP.
XX

AC AAZ34838:
XX

DT 28-FEB-2000 (first entry)
XX

DE Feline CD86 (B7-2) cDNA.
XX

KM CD86; B7-2; feline; cat; recombinant virus; vaccine;
KW Immunomodulator; tumour; cancer; therapy; ss.
XX

OS Felis domesticus.
XX

FH Key Location/Qualifiers
FT CDS 63..1052
ET CDS /*tag- a

PN MO9957295-A1.
XX

PD 11-NOV-1999.
XX

PF 30-APR-1999; 99MO-US09504.
XX

PR 01-MAY-1998; 98US-0071711.
XX

PA (SCHE) SCHERING-PLOUGH LTD.
PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.
XX

PI Winslow BJ, Cochran MD;
XX

DR WPI: 2000-062155/05.
DR P-PSDB: AAY32285.
XX

PT Novel recombinant virus useful as immunomodulators, particularly in
PS vaccines -
XX

XX Disclosure: Fig 3A; 230pp; English.

CC This is the nucleotide sequence of cDNA coding for feline CD86
CC (B7-2). The cDNA was isolated from feline peripheral blood
CC mononuclear cell cDNA by PCR. Manipulating the expression of CD28
CC or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC regulates T cell proliferation and cytokine release. The invention
CC relates to a recombinant virus that contains at least one foreign
CC nucleic acid, inserted into a nonessential genomic region, that
CC encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
CC immunogenic fragments, and is expressed when the recombinant virus
CC is introduced into a suitable host. The invention also provides:
CC a recombinant virus further comprising a foreign nucleic acid
CC encoding an immunogen derived from a feline pathogen; recombinant
CC viruses capable of enhancing an immune response to protect against
CC disease; recombinant viruses expressing antisense sequences,
CC capable of suppressing an immune response in a feline, e.g. for
CC treatment of autoimmune disease or transplant rejection; and
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used

CC to reduce or eliminate a tumour in cats.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
Query Match 98.3%; Score 979.2; DB 21; Length 1080;
Best Local Similarity 99.7%; Pred. No. 1.5e-274;
Matches 981; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGGCAATTTGTGACAGCACTATGGACTGAATCACTCTCTTGATGGCCCTCTG 60
Db 63 ATGGGCAATTTGTGACAGCACTATGGACTGAATCACTCTCTTGATGGCCCTCTG 122
QY 61 CTTCTGGTGTGTTCTTCCATGTAAGAGTCAGATATTTTCAACAGCTGGAACTGGCA 120
Db 123 CTCTCTGGTGTGTTCTTCCATGTAAGAGTCAGATATTTTCAACAGCTGGAACTGGCA 182
QY 121 TGGCAATTTTCAAAAGCTTCAAAACATTAAGCCCTGGATGGAGCTGTGATTTTGGCAGAGC 180
Db 183 TGGCAATTTTCAAAAGCTTCAAAACATTAAGCCCTGGATGGAGCTGTGATTTTGGCAGAGC 242
QY 181 CAGGATTAAGCTGTTCTGTATGAGATATTCAAGGCAAAAGAACCCCTCAAAATTTTCAT 240
Db 243 CAGGATTAAGCTGTTCTGTATGAGATATTCAAGGCAAAAGAACCCCTCAAAATTTTCAT 302
QY 241 CTCAAATATTAAGGCGGTGCAAGCTTTGCAAGAGCAACTGGACCTGAGACTCCACAAT 300
Db 303 CTCAAATATTAAGGCGGTGCAAGCTTTGCAAGAGCAACTGGACCTGAGACTCCACAAT 362
QY 301 GTTCAGATCAAGGACAAAGGCGACATATCACTGTTTCATTATTAAGGGCCCCAAAGGA 360
Db 363 GTTCAGATCAAGGACAAAGGCGACATATCACTGTTTCATTATTAAGGGCCCCAAAGGA 422
QY 361 CTAGTTCCCATGCAACCAATGAGTTCTGACCTATAGAGCTTGCAACTGAGCAACT 420
Db 423 CTAGTTCCCATGCAACCAATGAGTTCTGACCTATAGAGCTTGCAACTGAGCAACT 482
QY 421 GAAATTAAGTAACTTCTAATTAAGAACAGAAATTTCTGCAATCAATTAATTAAGCTGCTCA 480
Db 483 GAAATTAAGTAACTTCTAATTAAGAACAGAAATTTCTGCAATCAATTAATTAAGCTGCTCA 542
QY 481 TCTATTAAGGTTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTTAACACTGACAAATTTCA 540
Db 543 TCTATTAAGGTTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTTAACACTGACAAATTTCA 602
QY 541 ACTACTAAGTATGATCTGATGATGAAGAAATCTCAAAATTAATGAGACAGACTGTACAC 600
Db 603 ACTACTAAGTATGATCTGATGATGAAGAAATCTCAAAATTAATGAGACAGACTGTACAC 662
QY 601 GTTCTATCAGCTTGCCCTTTTCACTGCTCCCTGAAGCACAATGTAGCGTCTTTGTGCC 660
Db 663 GTTCTATCAGCTTGCCCTTTTCACTGCTCCCTGAAGCACAATGTAGCGTCTTTGTGCC 722
QY 661 CTGAACCTGAGACACTGAGAGATGCTGCTCCCTACTCTTCATTAATGAGACCAACT 720
Db 723 CTGAACCTGAGACACTGAGAGATGCTGCTCCCTACTCTTCATTAATGAGACCAACT 782
QY 721 AAGATTAAGAACCCCTGAACAAGGCCACTTCCCTGATTTGGCGCTGACTGTAAATTTT 780
Db 783 AAGATTAAGAACCCCTGAACAAGGCCACTTCCCTGATTTGGCGCTGACTGTAAATTTT 842
QY 781 GTTGTTTTTTGTGGAGTGTGCTCTTTAAACACTTAAGGAAAGAGAAAGACAGCCT 840
Db 843 GTTGTTTTTTGTGGAGTGTGCTCTTTAAACACTTAAGGAAAGAGAAAGACAGCCT 902
QY 841 GGCCCCCTCTCTGATGATGGAACCATCAAAAGGAGAGAAAGAGCAACAGACCAAC 900
Db 903 GGCCCCCTCTCTGATGATGGAACCATCAAAAGGAGAGAAAGAGCAACAGACCAAC 962
QY 901 GAAAGAGTACCATACCAAGTACTGAGAGATCTGATGAAGCCAGTGTATTATTAACATTTTG 960
Db 963 GAAAGAGTACCATACCAAGTACTGAGAGATCTGATGAAGCCAGTGTATTATTAACATTTTG 1022
QY 961 AAGACAGCTTCAGGCGACAAAGT 984

Query Match	Best Local Similarity	100.0%	Score 996:	DB 20:	Length 2830:
Matches 996:	Conservative	0:	Mismatches 0:	Indels	Gaps 0:
QY	1	ATGGGCAATTTGGAGAGCCATATGGAGCTGAGTCACTCCTCTGTATGGCCCTCTCG	60		
Db	2652	ATGGGCATTTTGACAGACACTATGGAGCTGAGTCACTCCTCTGTATGGCCCTCTCG	2593		
QY	61	CTCTCTGCTGTTCTTCATGAGATCAGCATATTTTACACAGACTGGAGACTGCCA	120		
Db	2592	CTCTCTGCTGTTCTTCATGAGATCAGCATATTTTACACAGACTGGAGACTGCCA	2533		
QY	121	TGCGCAATTTTACAAACCTCTCAAAACATTAACCGGATGAGCTGGTGTATTTTGGCAGC	180		
Db	2532	TGCGCAATTTTACAAACCTCTCAAAACATTAACCGGATGAGCTGGTGTATTTTGGCAGC	2473		
QY	181	CAGGATTAAGCTGGTCTGTATGATATTTTCAAGAGGCAAGAGAACCTCAAAATGTTCA	240		
Db	2472	CAGGATTAAGCTGGTCTGTATGATATTTTCAAGAGGCAAGAGAACCTCAAAATGTTCA	2413		
QY	241	CTCAATATTAAGGGCCGTCAAGCTTTTGCAGAGCAACCTGGACCCGTGACCTCCACAT	300		
Db	2412	CTCAATATTAAGGGCCGTCAAGCTTTTGCAGAGCAACCTGGACCCGTGACCTCCACAT	2353		
QY	301	GTTTCAGATTAAGGACAAAGGACATATTCACCTGTTTCATTCATTTTAAAGGGCCCAAGGA	360		
Db	2352	GTTTCAGATTAAGGACAAAGGACATATTCACCTGTTTCATTCATTTTAAAGGGCCCAAGGA	2293		
QY	361	CTAGTTCCTCATGCAACCAATAGTCTGACCTATCACTGCTTGTCTATCTCACTCAACCT	420		
Db	2292	CTAGTTCCTCATGCAACCAATAGTCTGACCTATCACTGCTTGTCTATCTCACTCAACCT	2233		
QY	421	GAAATTAAGCTTAACCTCTATATAGAAAGAAATTTGGCATCTTAATTTGACCTCTCA	480		
Db	2232	GAAATTAAGCTTAACCTCTATATAGAAAGAAATTTGGCATCTTAATTTGACCTCTCA	2173		
QY	481	TCATATCAAGGTTTACCAGAACCTTAAGAGATGTATTTTACGCTAAACCTGAGATTTCA	540		
Db	2172	TCATATCAAGGTTTACCAGAACCTTAAGAGATGTATTTTACGCTAAACCTGAGATTTCA	2113		
QY	541	ACTACTAATATGATCTCTGATGAGAAATCTCAAAATATATGTGACAGACCTGTAAC	600		
Db	2112	ACTACTAATATGATCTCTGATGAGAAATCTCAAAATATATGTGACAGACCTGTAAC	2053		
QY	601	GTTTCTATGAGCTTGGCTTTTTCAGTCCCTGGAAGCACACAAATGTGAGCGCTTTTGTGCC	660		
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QY	661	CTGAAGCTGGAGCACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGGACAACCT	720		
Db	1992	CTGAAGCTGGAGCACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGGACAACCT	1933		
QY	721	AAGGATTAAGAACCTTGAACAGGCACTTCTCTGTGATTTGCGGCTCTACTTGTAAATGTTT	780		
Db	1932	AAGGATTAAGAACCTTGAACAGGCACTTCTCTGTGATTTGCGGCTCTACTTGTAAATGTTT	1873		
QY	781	GTTGTGTTTTTGTGGAGTGTCTCTTTAAACACATTAAGAAAAGAAAGAAAGCAACCT	840		

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QY 61 CTCCTGCTGTTCTTCCATGAGAGTCAGCATATTTTCAAGAGCTGGAGACTGCCA 120
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Db 936 CTCCTGCTGTTCTTCCATGAGAGTCAGCATATTTTCAAGAGCTGGAGACTGCCA 877
QY 121 TGGCATTATTAACCTCCTCAAAACATTAAGCCTGGATAGCTGGATATTTTGGCAGAC 180
   |||
Db 876 TGGCATTATTAACCTCCTCAAAACATTAAGCCTGGATAGCTGGATATTTTGGCAGAC 817
QY 181 CAGGATAGCTGTTCTGTATGAGATATTCAGAGCAAGAGAACCTCAAAATGTTTCAT 240
   |||
Db 816 CAGGATAGCTGTTCTGTATGAGATATTCAGAGCAAGAGAACCTCAAAATGTTTCAT 757
QY 241 CTCAAATATTAAGGCGCTTACAGCTTTGACAGAGACAAGTGCACCTGAGACTCCACAT 300
   |||
Db 756 CTCAAATATTAAGGCGCTTACAGCTTTGACAGAGACAAGTGCACCTGAGACTCCACAT 697
QY 301 GTTGAGATCAAGAGCAAGGCGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 360
   |||
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QY 361 CTAGTCCCATGACCAAAATGAGTTTCAGCTATCAGTGCCTTCTTCACTTCACTCAACT 420
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Db 636 CTAGTCCCATGACCAAAATGAGTTTCAGCTATCAGTGCCTTCTTCACTTCACTCAACT 577
QY 421 GAATATACAGTACTTCTAATAGACAGAAATTTTGGCATCATTAATTTGACCTGCTCA 480
   |||
Db 576 GAATATACAGTACTTCTAATAGACAGAAATTTTGGCATCATTAATTTGACCTGCTCA 517
QY 481 TCATACAGGTTACCCAGAGACCTTAAGAGATGATATTTAGCTAAACATGAGATTTCA 540
   |||
Db 516 TCATACAGGTTACCCAGAGACCTTAAGAGATGATATTTAGCTAAACATGAGATTTCA 457
QY 541 ACTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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Db 456 ACTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 397
QY 601 GTTTCATGAGCTTGGCTTTTTCAGTCCCTGAGAGACAGAAATGAGAGCTTCTTGTGCC 660
   |||
Db 396 GTTTCATGAGCTTGGCTTTTTCAGTCCCTGAGAGACAGAAATGAGAGCTTCTTGTGCC 337
QY 661 CTGAACTGAGACACTGAGAGATGCTGCTCTCCCTACCTTTCATATATGATGACAACT 720
   |||
Db 336 CTGAACTGAGACACTGAGAGATGCTGCTCTCCCTACCTTTCATATATGATGACAACT 277
QY 721 AAGGATTAACACCTTGACAGAGGCCACTTCTGATTTGGCTGTACTTGTATGTTT 780
   |||
Db 276 AAGGATTAACACCTTGACAGAGGCCACTTCTGATTTGGCTGTACTTGTATGTTT 217
QY 781 GTTGTGTTTGTGGATGTTGCTCTTAAACACTAAGGAGAGAGAGAGAGAGAGAGAGCT 840
   |||
Db 216 GTTGTGTTTGTGGATGTTGCTCTTAAACACTAAGGAGAGAGAGAGAGAGAGAGAGCT 157
QY 841 GGGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
   |||
Db 156 GGGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 97
QY 901 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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Db 96 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 37
QY 961 AAGACAGCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
   |||
Db 36 AAGACAGCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1

```

```

DE Feline B7-2 protein encoding DNA.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Fells catius.
XX
XX MO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX MPI: 1999-571822/48.
XX
XX P-PSDB: AAY41079.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases
XX
XX Claim 1: Page 116-119; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX CC and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;
XX
XX Query Match 100.0%; Score 996; DB 20; Length 2830;
XX Best Local Similarity 100.0%; Pred. No. 3; 1e-279;
XX Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGCAATTTTGGAGAGACTATGGAGTCACTCTCTGATGAGGCTCTCTG 60
   |||
Db 179 AAGGCAATTTTGGAGAGACTATGGAGTCACTCTCTGATGAGGCTCTCTG 238
QY 61 CTCCTGCTGTTCTTCCATGAGAGTCAGCATATTTTCAAGAGCTGGAGACTGCCA 120
   |||
Db 239 CTCCTGCTGTTCTTCCATGAGAGTCAGCATATTTTCAAGAGCTGGAGACTGCCA 298
QY 121 TGGCATTATTAACCTCCTCAAAACATTAAGCCTGGATAGCTGGATATTTTGGCAGAC 180
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QY 241 CTCAAATATTAAGGCGCTTACAGCTTTGACAGAGACAAGTGCACCTGAGACTCCACAT 300
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Db 419 CTCAAATATTAAGGCGCTTACAGCTTTGACAGAGACAAGTGCACCTGAGACTCCACAT 478
QY 301 GTTGAGATCAAGAGCAAGGCGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 360
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Db 479 GTTGAGATCAAGAGCAAGGCGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 538
QY 361 CTAGTCCCATGACCAAAATGAGTTTCAGCTATCAGTGCCTTCTTCACTTCACTCAACT 420
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RESULT 3
 AA227929
 ID AA227929 standard; DNA; 2830 BP.
 XX
 AC AA227929;
 XX
 DT 20-DEC-1999 (first entry)
 XX

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 PS
 PS Claim 1, Page 123-124; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.

SQ Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;

Query Match 100.0%; Score 996; DB 20; Length 996;
 Best Local Similarity 100.0%; Pred. No. 1,9e-279;
 Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCAATTGTGACAGACATATGGAGCTACACTCTCTGATGGCCCTCTG 60
 DB 1 ATGGGCAATTGTGACAGACATATGGAGCTACACTCTCTGATGGCCCTCTG 60
 QY 61 CTCTCTGCTGTTCTTCATGAAGATCAAGCATATTTCAACAAGACTGGAACCTGCCA 120
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 QY 301 GTTCAGATCAAGAGAGGCGCATATCACTGTTTCATTTCAATTAAGAGGCGCCAAAGCA 360
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 QY 361 CTAGTTCCTCATGACCAATATGATCTGACCTATGCTGCTTCTCACTAGTCAACCT 420
 DB 361 CTAGTTCCTCATGACCAATATGATCTGACCTATGCTGCTTCTCACTAGTCAACCT 420
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 QY 721 AAGGATTAAGAGCCCTGAACAAAGCCACTTCTCTGATTTGGGCGTGTACTTGTATGTTT 780
 DB 721 AAGGATTAAGAGCCCTGAACAAAGCCACTTCTCTGATTTGGGCGTGTACTTGTATGTTT 780

QY 781 GTTGTTTTTGTGGAGTGTGCTCTTTAAACACTAAGAAAGAAAGAGACACCT 840
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 QY 841 GGCCCTCTCATGAATGTGAACCATCAAAAGAGAGAAAGAGACCAACAGACCAAC 900
 DB 841 GGCCCTCTCATGAATGTGAACCATCAAAAGAGAGAAAGAGACCAACAGACCAAC 900
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 QY 961 AAGACAGCTCAGGCGGACGACAAAGTACTACATTTT 996
 DB 961 AAGACAGCTCAGGCGGACGACAAAGTACTACATTTT 996

RESULT 2
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 ID AA27932 standard; DNA; 996 BP.

XX AA27932;
 AC 20-DEC-1999 (first entry)
 DT
 XX
 DE Complementary strand of feline B7-2 coding sequence.
 XX
 KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; feline;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 OS Felis catus.
 OS
 PN WO9947558-A2.
 PN
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-0506187.
 XX
 PF 19-MAR-1998; 98US-0078765.
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 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 PA
 XX
 PI Sim G, Yang S, Sellins KS;
 PI
 XX
 DR WPI; 1999-571822/48.
 XX
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 PS
 PS Claim 1, Page 124-125; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.

SQ Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;

Query Match 100.0%; Score 996; DB 20; Length 996;
 Best Local Similarity 100.0%; Pred. No. 1,9e-279;
 Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCAATTGTGACAGACATATGGAGCTACACTCTCTGATGGCCCTCTG 60
 DB 996 ATGGGCAATTGTGACAGACATATGGAGCTACACTCTCTGATGGCCCTCTG 937

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 150.574 Seconds
(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-28

Perfect score: 996
Sequence: 1 atgggcatctgtgacagcac.....acaaagtactaacatttt 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	996	AA227931	Feline B7-2 protei
2	996	100.0	996	AA227932	Complementary stra
3	996	100.0	2830	AA227929	Feline B7-2 protei
4	996	100.0	2830	AA227930	Feline B7-2 gene c
5	979.2	98.3	1080	AA234838	Feline CD86 (B7-2)
6	979.2	98.3	1080	AA234785	Cat CD86 (B7-2) cd
7	784.8	78.8	987	AA227915	Canine B7-2 protei
8	784.8	78.8	987	AA227916	Complementary stra
9	784.8	78.8	1897	AA227913	Canine B7-2 protei

C	10	784.8	78.8	1897	20	AA227914	Canine B7-2 gene c
	11	623.2	62.6	1050	21	AA49661	Pig costimulatory
	12	582.2	58.5	840	20	AA227923	Canine B7-2S prote
C	13	582.2	58.5	840	20	AA227924	Complementary stra
	14	582.2	58.5	1795	20	AA227921	Canine B7-2S prote
C	15	582.2	58.5	1795	20	AA227922	Canine B7-2S gene
	16	553	55.5	1424	21	AA229321	Human B7-2 gene
	17	553	55.5	1428	21	AA285873	Human B7-2 cDNA.
	18	553	55.5	2205	22	AAH72616	B70 type B antigen
	19	540	54.2	1130	16	AAQ81351	Human cervical can
	20	540	54.2	1130	18	AA749181	Human B lymphocyte
	21	540	54.2	1130	20	AAV55784	Human B lymphocyte
	22	540	54.2	1120	21	AA284049	Human B lymphocyte
	23	535	53.7	972	20	AAV83208	Human B lymphocyte
	24	535	53.7	972	24	AA25510	Human co-stimulat
	25	509	51.1	509	20	AA227934	Feline B7-2 protei
C	26	509	51.1	509	20	AA227934	Feline B7-2 gene (
	27	466.6	46.8	764	18	AA762939	Chimeric human/po
	28	434.6	43.6	831	19	AAV03230	DNA encoding CD86
	29	429.6	43.1	738	20	AAV80293	Human B7-2 extrac
	30	429.6	43.1	738	22	AAE89731	Nucleotide sequenc
	31	330	33.1	1261	16	AAE01046	Mouse B7-2 exons m
	32	329.6	33.1	1151	20	AAV55785	Mouse B7-2 antigen
	33	329.6	33.1	1163	18	AA749182	Mouse B lymphocyte
	34	329.6	33.1	1163	21	AA284050	Murine B lymphocyt
	35	328	32.9	1163	16	AAQ81366	Murine B lymphocyt
	36	291.6	29.3	942	19	AA799926	Rat CD86 coding se
	37	256	25.7	403	20	AAV89569	EST clone CR506.
	38	227.2	22.8	359	20	AA227935	Feline B7-2 protei
C	39	227.2	22.8	359	20	AA227935	Feline B7-2 gene (
	40	225	22.6	330	18	AA749197	Human B lymphocyte
	41	225	22.6	330	21	AA284082	Human B7-2 variabl
	42	214.6	21.5	430	21	AA200427	Human secreted pro
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	45	101.8	10.2	210	16	AAE01038	Human B7-2 exon 5.

ALIGNMENTS

RESULT 1
AA227931
ID AA227931 standard; DNA; 996 BP.
XX
AC AA227931;
XX
XX 20-DEC-1999 (first entry)
XX
DE Feline B7-2 protein coding sequence.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX
OS Felis catus.
XX
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX PD
XX 19-MAR-1999; 99WO-0506187.
XX
XX PF
XX 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX
XX (HESK-) HESKA CORP.
PA
XX
XX
XX Slim G, Yang S, Sellins KS;
PI
XX
XX WPI; 1999-571822/48.
DR
XX P-PSDB; AAV41079.
XX

Matches 180; Conservative 0; Mismatches 85; Indels 4; Gaps 2;

QY 731 ACCCTGACAAAGCCACTCTCTGATGCGCGCTGACTGTGAATGTTGTTGTTT 790
 Db 560 ACCCTGCCCGACACCATCTTGATTCACGCTGACTGCCGACGATTCATATGTG 501
 QY 791 GTGGATGTGTGCTTTAAACACTAAGCAAAAGAGAAGAGCAGCCTGGCCCTCTC 850
 Db 500 TGATGTTCTCTGTAGTATGCAATCGAAGAAAGAAAGCGCCTCGAACTCTT 441
 QY 851 ATGAATGTGAACCATCAAAAGGAGAGAAAGAGCAACAGCAACGAAGAGTAC 910
 Db 440 ATAAAGTGTG-AACCAACACAAATGAGAGAGAGTACAGACCAAGAAAGAGAA 382
 QY 911 CATACCAGTACCTGAGATCTGATGAAGCCAGTG---TATTACATTTTGAAGACAG 967
 Db 381 AAATCCATATACCTGAAAGATCTGATGAACCCAGCGCTGTTTAAAGTTGCAAGACAT 322
 QY 968 CCTCAGCGCAGCAAAAGTACTACACATTTT 996
 Db 321 CTTCATGCGCACAAAGTGATACATGTTT 293

RESULT 15
 AA946810/c 504 bp mRNA linear EST 23-JUL-1998
 LOCUS oq43c01.s1 NCI-CGAP_Kids Homo sapiens cDNA clone IMAGE:1589088 3'

DEFINITION similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN
 CD86 PRECURSOR ;, mRNA sequence.

ACCESSION AA946810
 VERSION AA946810.1 GI:3110205

KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 504)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

COMMENT Tissue Procurement: Christopher Koskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html

Insert Length: 1276 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amer sham

High quality sequence stop: 457.

Location/Qualifiers

FEATURES

source

1..504

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1589088"

/clone_1ib="NCI-CGAP_Kids"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGAGAAATTCGCGCGCAATATATTTTTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

"

136 a 94 c 109 g 165 t

BASE COUNT
 ORIGIN

Query Match 10.1%; Score 100.2; DB 9; Length 504;
 Best Local Similarity 76.8%; Pred. No. 3.3e-14;
 Matches 136; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 823 AGGAAGAAGACGACCGCTGCGCCTCTCATGATGTGAACCATCAAAAGGAGAGAAA 882
 Db 477 AAGAAGAAGAAGCGCGCTCGCACTCTTAATAATGTGAACCAACAAATGAGAGGAGAA 418
 QY 883 GAGAGCAACAGACCAAGCAAGAGAGTACCATACGACGTAAGATGATGATGAAGCC 942
 Db 417 GAGAGTGAACGACCAAGAAAGAGAAAAATCCATATACCTGAAGATCTGATGAAAC 358
 QY 943 GAGTG---TATTACATTTTGAAGACAGCCTCAGGCGCAAAAGTACTACATTTT 996
 Db 357 CAGCGTGTTTTAAAGTTGAGAGACATCTCATGCGCAAAAGTGAATACATGTTT 301

Search completed: October 20, 2002, 04:29:59
 Job time : 1199.05 secs

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Db 480 TGGAAATGAGAGAGAGAGAGCGGCGCTCGCAACTTATTAATGTGGAACCAACAATG 421
Qy 874 GAGAGAAAAGAGAGCAACAGACCAAGAGTACCATCCAGTACCTGAGAGATCT 933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 GATGAGGAAGAGAGTGAAGAGAGCAAGAAAAGAAAATCATATACCTGAAAGATCT 361
Qy 934 GATGAAGCCAGTGTG--TATTACATTTTGAAGAGAGCGCTCAGGGGACAAAAGTACTACA 990
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 GATGAAGCCAGTGTGTTTAAAGTTGGAAGAGATCTTCATGCGACAAAAGTATACA 301
Qy 991 CATTTT 996
    |||||
Db 300 TCTTTT 295

RESULT 13
Bg001664 347 bp mRNA linear EST 24-JAN-2001
LOCUS RC4-GN0067-151100-016-b07 GN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg001664
VERSION Bg001664.1 GI:12440219
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 347)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-GN0067-
151100-016-b07&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 347.
Location/Qualifiers
source
1. 347
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/db_xref="taxon:9606"
/clone_id="GN0067"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal
; Site_2: Sma1; A mini-library was made by cloning
products derived from ORESRS PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 109 a 75 c 75 g 88 t
ORIGIN
Query Match 11.0%; Score 109.8; DB 10; Length 347;
Best Local Similarity 62.6%; Pred. No. 1,4e-16;
Matches 171; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 679 GAGATGCTGCTCTCTACCTTCAATATATAGTACACACACTAAGTAAGTAAGCCCTGAA 738

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Db 50 GACAAGACGGCGCTTTTATCTTACCTTCTCTACAGAGTTGAGAGCCCTCAGCCTCCC 109
Qy 739 CAAGCCCACTTCTCTCTGATTCGGCGCTGTACTGTATGTTGTTGTTTGTGGATG 798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 CCAAGCCACATCTCTTGGATTACAGCTGTACTTCAACACTTATATATCTGATGTT 169
Qy 799 GTCTCTTTTAAACACTAAGAAAAGAGAGAGAGCGCTGCGCCCTCATGATG 858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 TTCTGTCTAATCTATGGAATGGAAGAGAGAGAGCGCTGCGCAACTTTTAAATGT 229
Qy 859 GAAACCATCAAAAGAGAGAGAGAGAGCAACAGACCAAGAGAGTACCATACAC 918
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Db 230 GGAACCAACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
Qy 919 GTACCTGAGATCTGTATGTAAGCCCACTAT 951
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Db 290 ATACCTGAAGATCTGTATGTAAGCCCACTAT 322

RESULT 14
A1093604 570 bp mRNA linear EST 10-NOV-1998
LOCUS C082209.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1634297 3' similar to SW:CD86_HUMAN P42081 r LYMPHOCYTE
ACTIVATION ANTIGEN CD86 PRECURSOR ;, mRNA sequence.
ACCESSION A1093604
VERSION A1093604.1 GI:3432580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 570)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgrabs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 801 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 400.
Location/Qualifiers
source
1. 570
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/db_xref="taxon:9606"
/clone_id="IMAGE:1634297"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pTZ19D-pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were used as tracer.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneids: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740939 Subtraction by Bento
Soares and M. Fatima Bonaldi."

BASE COUNT 150 a 107 c 134 g 179 t
ORIGIN
Query Match 10.5%; Score 105; DB 9; Length 570;
Best Local Similarity 66.9%; Pred. No. 2.2e-15;

```


Db	653	ACAGACATTACAGAACTGT	654	
RESULT 9				
LOCUS	AM427922		257 bp	linear
DEFINITION	64549 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.			EST 25-APR-2001
ACCESSION	AM427922			
VERSION	AM427922.1	GI:6955869		
KEYWORDS	EST.			
SOURCE				
ORGANISM	Bos taurus			
COV	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea; Bovidae; Bovinae; Bos.			
REFERENCE				
AUTHORS	Smith,T.P.L., Grosse,W.M., Fekling,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pertes,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.			
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle			
JOURNAL	Genome Res. 11 (4), 626-630 (2001)			
MEDLINE	21180013			
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. PCR primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCACAGTCACGAC BLAST: 30 row: G column: 20 Seq primer: ATTGAGGACACTATG. Location/Qualifiers 1..257 /organism="Bos taurus" /db_xref="taxon:9913" /clone_id="MARC 3BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI; library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal Longissimus muscle."			
FEATURES				
SOURCE				
BASE COUNT	80 a	64 c	52 g	61 t
ORIGIN				
Query Match	18.0%	Score 179.2;	DB 9;	Length 257;
Best Local Similarity	81.2%	Pred. No. 1.1e-33;		
Matches 208; Conservative	0;	Mismatches 48;	Indels 0;	Gaps 0;
QY	115	CTGGCATGCCCTTTTACAACTCCAAACAAACATTAAGCCGTGATGAGCTGATATTTGG	174	
Db	2	CTGGCATGCCCTTTTCCAAACACCCAAACCTCGACGCAAGCTGTATATTTTGG	61	
QY	175	CAGGACCAAGATTAAGCTGTCTGTATGACATATTATTCAGAGCAAGAACCTTCAAAT	234	
Db	62	CAGATTCAGATTAAGTGTCTCTATGAGCTATTTCAAAGGCCAAGAAACCCCAATAT	121	
QY	235	GTTATCTCAATATTAAGGCGCTACAGCTTTACAAAGCAACATGGACCTGAGACTC	294	
Db	122	GTTAATCCCAAGTATATAAGGCCGACCAAGCTTGACCAAGAGAGCTGGACCTGAGACTC	181	
QY	295	CACAAATGTGACATCAAGGACAAGGACCATATACGTCTTCATTCATTAATAAGGCC	354	
Db	182	CACAACTTCATTAATCAAGACACAGGCTGTATTAAGTTTTCATTCATTAAGAGATCC	241	

QY	355	AAAGACGTAGTTCCCA	370
Db	242	CAAGATGTTGGTTCCA	257
RESULT	10		
LOCUS	AWS16826		
DEFINITION	x904h01.x1 Soares_NHCEC_cervical_tumor Homo sapiens CDNA clone IMAGE:2748913.3' similar to SW:CD86_HUMAN P42081 T LYMPHOCTE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.	496 bp	mRNA linear EST 03-MAR-2000
ACCESSION	AWS16826		
VERSION	AWS16826.1	GI:7154992	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	I (bases 1 to 496)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Glpco High quality sequence: 458.		
FEATURES	Location/Qualifiers		
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	/tissue_type="tumor"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: cervix; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTTACCATTCTGAAGTGGAGCGGCCGCAGAGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized; constructed by Bento Soares and M.Patrina Bonaldo."		
BASE COUNT	156 a 102 c 93 g 145 t		
ORIGIN			
Query Match	12.5% Score 124.2; DB 9; Length 496;		
Best Local Similarity	63.9%; Pred. No. 4.1e-20;		
Matches 205; Conservative	0; Mismatches 113; Indels 3; Gaps 1;		
Y	679	GAGATGTCGTCCTCTCCACTTTTCATATAGATGCACAACTAAGATTAAGAAGCCCTGAA	738
Db	59	GACAAGAGCGCGCTTTATATCTTCACTTTCTCTATAGAGCTTGAGAACCCCTCACCC	118
Y	739	CAGGCCACTTCTCTCTGATTTGGCGCTGTACTTGTAAATGTTGTTGTTTGTGGCATG	798
Db	119	CCAACCAACATCTCTGGATTACAGCTGTACTTCCACAGTTATATATGTGTGATGTT	178
Y	799	GTCGCTTTAAACATAAGAGAAAAGAGAAAGAAAGAGAGCCCTGCCCTCTGCATGAATG	858
Db	179	TTCTGTCTAATTTCTATGGAATGGAAGAGAAAGAGCGGCTCGCAACTCTTATTAATGT	238
Y	859	GAACCATCAAAAGGGAGAGAAAAGAGAGCAACAGACCAACGAAAGTAGTACCATACAC	918
Db	239	GGAACCAACACATGAGAGGAGAGAGAGTGAACACAGACCAAGAAAAGAAAAAATCAT	298
Y	919	GTACCTAGAGATCTGATGAAGCCCATG---TATTACATTTTGAAGACAGCCTCAGGC	975
Db	299	ATACCTGAAGATCTGATGAAGCCCATGTTTAAAGTTTGAAGACATCTTATGTC	358

OY	613	TTCGCTTTTTCAGTGCCCGTAGACACAACTGTGCAGCGTCTTTTGTGCCCTGAACATCGAG	672
Db	393	GTTGTTCTTTCCTCATCCTCCGAGCAAAATGTGACACAATNGTGTGTCTCTCGAACACTTGAG	334
OY	673	ACATGAGAGA---TGCCTGCTCCCTACCTCTTCATTATAGATGACCAACCTAANGATMAA	729
Db	333	CCAACGACAGACACTGCTTTTCTCCTACCCTGTATAATATGATGCAAAGCACCTGTGCNA	274
OY	730	GACCTGGAACAAGCGCACTTCTCTGGATTGGCGCTGTACTTGTATGTTTTGTGTGTTT	789
Db	273	CCCCCTGTCCAGACCAACATCCTNNGATTTGGAGCTTACTTGTAACAAGTGTGCTGG	214
OY	790	TGTGGGATGTTGCTCTTTAAAAACTATAGAAAAGAAAGAACACAGCCTTGCCCTCT	849
Db	213	TGTGGGATGTTGCTCTTTGTAACTAATGAAAGAAAGAAACAAACACAGCTGGCCCTCT	154
OY	850	CATGAAT---GTGAACCATCAAAAGGAGAGAAAGAGAGCAACAGCAACCAAGMAA	906
Db	153	AATGAATGTGTGGAACCATCAAAATGAAACAGGAAGCGAGTGAACAACTAAGAACAG-	95
OY	907	GTACCAATCCACGTACTGAGAGATCTGATGAAAGCCCAGTG--TATTAACATTTTGAAG	963
Db	94	-----AAGTCCATGAACGATCTGATGTATGCGCCAGTGTGATTTAATTTTNAG	45
OY	964	ACAGCTCAGGAGCAAAAGTACTACATTTT	996
Db	44	ACAGCTCAGATGACAAACGTACTACAGATTTT	12
RESULT 8	B635605	B635605	654 bp mRNA linear EST 26-OCT-2001
LOCUS	B635605	Riken full-length enriched, 0 day neonate thymus Mus	
DEFINITION	B635605	musculus cDNA clone A430076L06 5', mRNA sequence.	
ACCESSION	B635605		
VERSION	B635605.1	GI:16471650	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 654)		
	Arakawa,T., Carlinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.		
	, Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda,		
	, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,		
	Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakiki,		
	, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,		
	Tegami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,		
	Muramatsu,M. and Hayashizaki,Y.		
	Muramatsu Mouse ESTs (Arakawa,T., et al. 2001)		
TITLE	Unpublished (2001)		
JOURNAL	Contact: Yoshihide Hayashizaki		
COMMENT	Laboratory for Genome Exploration Research Group, RIKEN Genomic		
	Sciences Center(GSC), Yokohama Institute		
	The Institute of Physical and Chemical Research (RIKEN)		
	1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan		
	Tel.: 81-45-503-9222		
	Fax: 81-45-503-9216		
	Email: genome-res@gsc.riken.go.jp,		
	URL:http://genome.gsc.riken.go.jp/		
	Carlinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh		
	, M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new		
	genes. Genome Res. 10 (10), 1617-1630 (2000)		
	waghi,K., Fujiwake,S., Inoue,K., Togawa,Y., Ikawa,M., Ohara,E.,		
	Wachiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra		
	,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and		
	Hayashizaki,Y.		
	RIKEN integrated sequence analysis (RISA) system--384-format		
	sequencing pipeline with 384 multichipillary sequencer. Genome Res.		
	10 (11), 1757-1771 (2000)		

	Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
	Rondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamakita, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
	Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
	e mouse tissues.
FEATURES	
Source	location/qualifiers
	1..654
	/organism="Mus musculus"
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	/clone="AA30076L06"
	/clone_1lb="RIKEN full-length enriched, 0 day neonate thymus"
	/tissue_type="thymus"
	/dev_stage="0 day neonate"
	/lab_host="DH10B"
	/note="Site:1: Sali; Site:2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
	GAGGAGAGAAGATCCACAGACGCTTTTGTTCCTTTTTVVN 3'/, cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAATTAAATTAATCCCCCCCCCCC 3'/. cDNA was cleaved with xhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT	148 a 151 c 152 g 202 t 1 others
ORIGIN	
Query Match	20.2%; Score 201.4; DB 9; Length 654;
Best Local Similarity	70.5%; Pred. No. 4,1e-39;
Matches 268; Conservative	0; Mismatches 112; Indels 0; Gaps 0;
OY	15 CAGCATTGGGACTGAATCACACTCTCTTGATGAGCCCTCCGCTCTCGGTTTC 74
Db	275 CTGCACCATGGGCTTGCGCAATCTTATCTTTGTGACAGTCTTGCTGATCTAGATCGT 334
OY	75 TTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAACACTGCCATCCATTATACAA 134
Db	335 TTCCGTGAGAACGCAAGTTATTTCANIGGAGCTSCATATCTGCCGTCGCCATTACAAA 394
OY	135 CTCCTAAAAACATAAGCCCTGATGAGCTGTGATATTTTGGCAGACCAGGATTAAGCTGGT 194
Db	395 GGCTCAAAACATTAACCCCTGAGTGAAGTAGTATTTTGGCAGGACCCAGCAAAGTTGGT 454
OY	195 TCTGTATAGATATTTCAGAGCAAGAAAGAACCCCTAAATATGTCATCTCAATATTAAGG 254
Db	455 TCTGTACGACGACATTTTGGGACACAGAAACTGATATGTGTGAATGGCAAGTACTGNG 514
OY	255 CGGTACAAGCTTTGCAAGAGCAACTGGACCCCTGAGACTCACAATGTTCTGAGATCAAGA 314
Db	515 CCGCAGCGAGCTTTTGACAGGAAGAACTGGACCTCAAGCTTCAACATGTTCTGATCAAGA 574
OY	315 CAAGGACACATATCCTCTTCATTCATTATTAAGGGCCCAAGAGACTAGTCCATGCCA 374
Db	575 CATGGCGTCGTATGATGTTGTTTATACAAAAAAGCCACCCACAGAGATCAATTAATCTCC 634
OY	375 CCAATGAGTCTCGACTAT 394

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Oy 622 TCAGTCCGTGAAG 634
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Db 684 TCATCCCGGATG 696

RESULT 6
BM089797
LOCUS 578 bp mRNA linear EST 19-NOV-2001
DEFINITION 503647 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM089797
VERSION BM089797.1 GI:17000425
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 578)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
CONTACT: Smith RPL
USDA, ARS US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 5 row: D column: 18
Seq primer: ATTGTAGTGACCATGAC.
FEATURES
source
1..578
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone.lib="MARC 2B0Y"
/tissue.type="pooled"
/lab.host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled tissue from testis, thymus,
semilendonsus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 170 a 150 c 120 g 137 t 1 others
ORIGIN
Query Match 26.1%; Score 259.6; DB 10; Length 578;
Best Local Similarity 76.9%; Pred. No. 1.9e-53;
Matches 339; Conservative 0; Mismatches 80; Indels 22; Gaps 1;

Oy 17 GCACATATGGGAGTCACTCTCTGTATGATGGCCCTCTGCTCTGTGTTCTT 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 GCACATATGGGAGTCACTCTCTGTATGATGGCCCTCTGCTCTGTGTTCCACG 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 77 -----CCATGAAGAGTCAACATATTTCAACAAGACTGGAGAA 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 TTCCTTTTCAGGTGCTGCTTCCTTNGAAAATCATGCTTCTTTCAAGAGACTGAGAA 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 115 CTGCATATGCCATTTTACAACACTCAAAACATTAAGCTGGATGAAGCTAGTATTTGG 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 CTGCATATGCCATTTTCAACACCAAAACCTCAAGCTGAGCAAGCTGGTATATTTGG 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 175 CAGGACCAAGATTAAGCTGTTCTGTATGATATTCAGAGGCAAGAGAACCTCAAAAT 234
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Db 317 CAGATTCAGAAATTAAGTTGGTTCTCTATGAGCTATTCAAGGCCAAGAGCAATTAAT 376
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Oy 235 GTTATCTCAATATTAAGGGCGGTACAAAGCTTTCACAAAGCAATGAGACCTGAGACT 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 GTTAATCCCAAGTATTAATGAGCGGCACAGACTTTTACCAAGACAGTTGGACCTTGAGCTC 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 295 CACAATGTTTCAGATCAAGAGCAAGGCGACATATCACTGTTTCATTATTAAGGGCCC 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 CACAACGTTCAATCAAAAGACACAGGCGTGTATCAATGTTTCATTCACATAGAAAGCTCC 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 355 AAAGAGCTAGTTCCCATGACCAACCAATGATGCTGACCTATCACTGCTTGAATTAGT 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 CAGGATGTTTCATTCATCCACAGATGAGTTGACCTGATAGTGTGGCTAACTTCACTGAGT 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 415 CAACCTGAATTAACGTAAT 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 CAACCAAGAAATTAACGTAATT 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
AA056905/c
LOCUS 512 bp mRNA linear EST 18-SEP-1996
DEFINITION EST224F Pig Spleen lambda gt 11 Library (Clontech cat # PL1006b)
Sus scrofa cDNA clone SPL224 forward similar to L25259 CTUA4
counter-receptor , human, mRNA sequence.
AA056905
ACCESSION AA056905.1 GI:1549545
VERSION AA056905
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 512)
AUTHORS Tugale,C.K., Wahls,S. and Schmitz,C.
TITLE Tugale,C.K., Wahls,S. and Schmitz,C.
JOURNAL Unpublished (1996)
COMMENT Contact: Tugale CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: oktugale@iastate.edu
PCR PRIMERS
FORWARD: TGGCGAGAGCTCCTCG
BACKWARD: GACCGCGCTCAGCT
Insert length: 950 Std Error: 50.00
Seq primer: TGGCGAGAGCTCCTCG.
FEATURES
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/db_xref="taxon:9823"
/clone.lib="SPL224"
/clone.lib="Pig Spleen lambda gt 11 Library (Clontech cat
# PL1006b)"
/tissue.type="spleen"
/dev_stage="adult"
/note="Oligo (dtr) primed"
BASE COUNT 125 a 106 c 114 g 163 t 4 others
ORIGIN
Query Match 24.7%; Score 245.8; DB 9; Length 512;
Best Local Similarity 74.3%; Pred. No. 4.7e-50;
Matches 381; Conservative 0; Mismatches 111; Indels 21; Gaps 5;

Oy 493 TACCAGAACTAAGAGATATATTTTCAGCTAAACACTGAGATTAACCTAGTAT 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 TACCAGAAACCCAGAGATGATATATGTTGCTAATATCGAAGATTCACACCTGAGACAT 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 553 GATCTGCATGAAGAATATCAAAATATATGTGACAGAACTGTACAGCTTTCTATCAGC 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 GATCTGCATGAAGAATATCAAAATATACATCAC-GGANTTTACATGTATATCAGG 394
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AA056906	AA056906	448 bp	mRNA	linear	EST 18-SEP-1996
LOCUS	EST222R Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)				
DEFINITION	Sus scrofa cDNA clone SPL224 reverse similar to L25259 cTL4 counter-receptor, human, mRNA sequence.				
ACCESSION	AA056906				
VERSION	AA056906.1	GI:1549546			
KEYWORDS	EST.				
SOURCE	pig.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
AUTHORS	1 (bases 1 to 448)				
TITLE	Tuggle,C.K., Wahls,S. and Schmitz,C.				
JOURNAL	Expressed Sequence Tags from Pig Spleen				
COMMENT	Unpublished (1996) Contact: Tuggle CK Molecular Genetics Laboratory, Department of Animal Science Iowa State University 201 Kildee Hall, Ames, IA 50011-3150, USA Tel: 5152944252 Fax: 5152942401 Email: cktuggle@iastate.edu PCR Primers FORWARD: TGCGGCGACTGCTG BACKWARD: GACCGCGCTCAGCT Insert Length: 950 Std Error: 50.00 Seq primer: GACCGCGCTCAGCT. Location/Qualifiers 1. 448 /organism="Sus scrofa" /db_xref="taxon:9823" /clone="SPL224" /clone_lib="Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)" /tissue_type="spleen" /dev_stage="adult" /note="Oligo (dT) primed"				
BASE COUNT	126 a 116 c 89 g 116 t				1 others
ORIGIN					
Query Match	33.0%; Score 328.6; DB 9; Length 448;				
Best Local Similarity	86.0%; Pred. No. 1.9e-70;				
Matches 388; Conservative 0; Mismatches 59; Indels 4; Gaps 2;					
Oy	CTCCTTGATGGCCCTCGCTCTCGTGTTCATG-AAGAGTCAGACATATTT	98			
Db	1 CTGTTGGAGTGCCTCGCTCTCGTGTTCATG-AAGAGTCAGACATATTT	60			
Oy	99 CACCAAGCTGGAACATGCCATGCCATTTTACAAACTCTCAAAACATAGCGCTGATTA	158			
Db	61 CAATGAGACTGGAAACATGCCGTCCTTTTAAACACTGCAAAACCTAAGCGTGGATGA	120			
Oy	159 GCTGTGATATTTTGGAGAGCAGATAGCTGTTCTGATAGATATTCAGAGGCCAA	218			
Db	121 GCTGTCATATTTTGGAGAGCAGATAGCTGTTCTGATAGATATTCAGAGGCCAA	180			
Oy	219 AGAGAACCTCAAAATGTCATCTCAAAATTAAGGCCGCTACAAAGCTTTGACAGAGCA	278			
Db	181 AGAGAGCTCATATATTTTATTCACAGTATATGGTCCGACAGAGCTTTGACAGGCCA	240			
Oy	279 CTGGAACCTGAGACTCCACAATGTTTCAGATCAAGACAAAGGACATATCTGTTTCAT	338			
Db	241 CTGGAACCTGAGACTCCACAATGTTTCATCAAGACAAAGGCGCTCATTCATGTTTCAT	300			
Oy	339 TCATTTAATTAAGGCGCAAGAGACAGTATCCATGCAAGAGTTCGACCTATCAGT	398			
Db	301 CCATCATTAAGGCGCGAGTATGTTCTATTCACACAGATGATGTTGACCTATCAGT	360			
Oy	399 GCTTGTAACTTCAAGTCAACCTGAATTAACAGTAACTTCAATAGACAGAAATTCG	458			
Db	361 GCTTGTAACTTCAAGTCAACCTGAATTAACAGTAACTTCAATAGACAGAAATTCG	419			

Oy	459	CATCATTAATTTGACCGCTCATCTATCA	489.	
Db	420	--TCATTAATTTGACCTGCTCATCTACACA	448	
RESULT 4				
BB631711				
LOCUS				
DEFINITION	BB631711 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A13009JH03 5', mRNA sequence.			
ACCESSION	BB631711			
VERSION	BB631711.1	GI:16468418		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 629)			
TITLE	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyo,T., Muramatsu,M. and Hayashizaki,Y.			
JOURNAL	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
COMMENT	Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) Wagti,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,Y., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.			
FEATURES				
source	1. 629 /organism="Mus musculus" /db_xref="taxon:10090" /clone="A13009JH03" /clone_lib="RIKEN full-length enriched, 16 days neonate thymus" /tissue_type="thymus" /dev_stage="16 days neonate" /lab_host="DH10B" /note="Site.1: Sali; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia			

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LOCUS	BI824940				
DEFINITION	603032254r1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173789 5', mRNA sequence.				
ACCESSION	BI824940				
VERSION	BI824940.1	GI:15936490			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
REFERENCE	1 (bases 1 to 655)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D.				

QY	17	GCACATGAGGACCTAGTCACACACCTCCTTGATGAGGCCCTCCAGCTCCTCGAGTTCCT	76
Db	161	GCACATGAGGACCTAGTACACCTTCTCTTTGATGAGCCCTCCTGCTCTCTGGTGTCTC	220
QY	77	CCATGAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGTCATTTACAACCT	136
Db	221	CTCTGAGAGATTCACAGCTTATTTTCATGAGACTGCAGACCTGCCATGTCATTTGCAAACT	280
QY	137	CTCAAAACATTAAGCCTGGATGAGCTGGTAGATTTTGGGAGGCCAGGATTAACCTGGTTC	196
Db	281	CTCAAAACCAAAAGCCTTAGTGAGCTAGTATGATTTTGGCGAGCCAGGAAACCTTGGTTC	340
QY	197	TGTATGAGATATTTCAAGAGCCAAAGAACCCCTCAAAAATGTTTCATCTCAATATTAAGGCC	256
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QY	257	GTAACAACCTTTGACAAGGACCACTGGGACCCCTGAGACTCCCAATGTTCCAGATCAAGGACA	316
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QY	317	AGGGCACAATATCACTGTTTTCATTTCATATATTAAGAGGCCCAAGAGACTAGTCCCATGCACC	376
Db	461	AGGCTTGTATCAATGTATCATCATCATCAAAAAGCCACAGGAATGATTCGATCCACACC	520
QY	377	AAATGATTTCTGACCTTACAGTGTCTTGCTTAACCTTCACGTCAACCTGGAATTAACGTAACCT	436
Db	521	AGATGAATTCGACCTGTCAGTGTGTGCTTAACCTTCACCTCAACCTGGAATTAAGTCCAAATTT	580
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Db	581	CTAATTAACGAAAA---TGTGTACATACATTTTGACCTCTCATCATATTAACAGGTTACC	637
QY	497	CAGAACCTAAGAGATGC	513
Db	638	CAGAACCTAAGAGATGC	654

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1187.05 Seconds
(without alignments)
11324.679 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_estbhm:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
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12: gb_gss:*
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14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	399.2	40.1	753	10	BI906246 603063172
2	348.2	33.0	655	10	BI824940 603032554
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4	276.4	27.8	629	9	BB631711 BB631711
5	268.6	27.0	1002	10	BF137460 601780644
6	259.6	26.1	578	10	BM088797 503647 MA
7	245.8	24.7	512	9	AA056905 EST724R P
8	201.4	20.2	654	9	BB635605 BB635605
9	179.2	18.0	257	9	AA427922 64549 MAR
10	124.2	12.5	496	9	AA516826 xq04h01.x
11	120.4	12.1	514	10	BF171298 PC12416 M
12	111.6	11.2	343	10	BF064222 7157b02.x
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14	105	10.5	570	9	AI093604 ou82b09.s
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20	58.8	5.9	466	10	BI132458	BI132458 RC3-NT011L
21	46.6	4.7	695	10	BI767024	BI767024 603054234
22	45	4.5	391	9	AI632116	AI632116 ts85b01.x
23	43.2	4.3	378	9	AA973397	AA973397 o044a04.s
24	42.2	4.2	1032	10	BI762625	BI762625 603048179
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26	41	4.1	1101	9	AL513871	AL513871 AL513871
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29	40.2	4.0	741	12	A2175416	A2175416 SP_0132.A
30	39.8	4.0	303	9	AI565637	AI565637 t04109.x
31	39.6	4.0	919	10	BF036274	BF036274 601459416
32	39.2	3.9	629	12	A2358039	A2358039 IM0100601
33	39.2	3.9	989	12	CNS00K2D	AL077036 Drosophila
34	39	3.9	706	12	A0855359	A0855359 CPG1892B
35	38.8	3.9	316	9	AL514579	AL514579 AL514579
36	38.8	3.9	764	12	BH467265	BH467265 B08C21TF
37	38.8	3.9	1101	12	CNS0039V	AL063956 Drosophila
38	38.6	3.9	611	9	AI888372	AI888372 w30607.x
39	38.6	3.9	854	12	BH181390	BH181390 018-D_11-
40	38.6	3.9	854	12	CNS07NOY	AL1618340 T7 end of
41	38.6	3.9	1101	12	CNS04529	AL305838 Tetradon
42	38.4	3.9	928	12	CNS00DKY	AL071865 Drosophila
43	38.2	3.8	1126	12	CNS04RCT	AL303734 Tetradon
44	38	3.8	1101	12	CNS00D03	AL075325 Drosophila
45	37.8	3.8	1035	12	CNS002D5	AL097523 Drosophila

ALIGNMENTS

RESULT 1
BI906246 753 bp mRNA linear EST 16-OCT-2001
603063172F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5212648 5',
LOCUS
DEFINITION
BI906246
ACCESSION
BI906246
VERSION
BI906246.1 GI:16168907
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 753)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inceye Genomics, Inc.
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 719.
Location/Qualifiers
1. 753
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/clone_1b="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dt primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

FEATURES

source

Sun Oct 20 08:15:57 2002

us-09-646-561-28.rge

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Qy	914	ACCGACGACCTGAGAGATGTGATGAGAGCCCAAGG---TATTAACTTTTGGAAACAGCT	970
Db	1008	TCCATTACTCGAAGAGTTCGATGAGAAAGCCACAGCGTGTTTTAAAGTTGAGACATCTT	1067
Qy	971	CAGCGGCAAAAAGTACTACACATTTT	996
Db	1068	CATCGGACAAAAGTACTGTTT	1093

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Job time : 1373.8 secs
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QY 557 CTGTGATGAAGAATCTCAAAATATATGTGACAGAACTGTGACAACTGTTCTATCAGCTTGC 616
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QY 617 CTTTTCAGTCCCTGAAG---CACACATGTGAGCGCTTTTGTGCCCTGAAGACTGAGA 673
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Db 968 CATGCCAAGAAAGTATACATGTTT 993

RESULT 15
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LOCUS HUMB72A
DEFINITION Human CTLA4 counter-receptor (B7-2) mRNA, complete cds.
ACCESSION L25259
VERSION L25259.1 GI:416368
KEYWORDS CTLA4 counter-receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1112)
Freeman,G.U., Gribben,J.G., Boussiotis,V.A., Ng,J.W., Restivo,V.A.,
Jr., Lombard,D.A., Gray,G.S., and Nadler,L.M.
Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human
T cell proliferation [see comments]
Science 262 (5135), 909-911 (1993)
JOURNAL 94053735
MEDLINE
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BASE COUNT 346 a 237 c 230 g 299 t
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Query Match 54.28; Score 540; DB 9; Length 1112;
Best Local Similarity 75.48; Pred. No. 4e-136;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
QY 17 GCATTGAGGAGTACAGTACACTCCCTGATGAGGCGCTCCGCTGCTGCTGCTTCT 76
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QY 137 CTCAAAACATAGCCTGATGAGCTGGTATTTTGGGAGACAGAGATAGCTGCTT 196
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QY 197 TGTATGATATTCAGAGAGCAAGAAACCTCAAAATGTTTCATCTCAATATTAAGGGCC 256
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Db 828 CTCCCCCAAGACACATTCCTTGATTTACAGCTGCTTCCAAAGTATATATGTTGA 887
QY 794 GGATGCTGCTTTTAAACACTAAGAGAAAGAAAGAAAGACAGCGGCCCTCATG 853
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Db 888 TGGTTTTCCTCTAATTTCTATGGAATGAAAGAAAGAAAGAGCGGCTGCAACTCTTATA 947
QY 854 AATGTGAACCATCAAAAGGAGAGAAAGAGAGCAACCAAGCAAGAAAGATACCAT 913
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DEFINITION Sequence 33 from patent US 6251627.
ACCESSION AR159758
VERSION AR159758.1 GI:16222530
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6251627-A 33 26-JUN-2001;
FEATURES
  source Location/Qualifiers
    1..1002
BASE COUNT 309 a 215 c 203 g 275 t
ORIGIN

Query Match 54.2%; Score 540; DB 6; Length 1002;
Best Local Similarity 75.4%; Pred. No. 4e-136;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACATATGGAGCTGAGTACACTCTCTGTGATGGCCCTCTGCTCTGTGTTCTT 76
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QY 77 CCATGAAGATCAAGCATATTTCAACAAGACTGGAACTGCCATTTTACAAACT 136
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QY 137 CTCAAAACATAGACCTGGATGAGCTGTGATATTTTGGCAGACAGCATAGCTGTTG 196
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DB 677 ---AGAGCGCGCTTTATCTTCACTTCTCTATAG-----AGCTTGAAGACCTTCAGC 727
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QY 971 CAGCGACAAAGATCACTACATTTT 996
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RESULT 14
LOCUS AR160450 1002 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 33 from patent US 6255073.
ACCESSION AR160450
VERSION AR160450.1 GI:16224366
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6255073-A 33 03-JUL-2001;
FEATURES
  source Location/Qualifiers
    1..1002
BASE COUNT 309 a 215 c 203 g 275 t
ORIGIN

Query Match 54.2%; Score 540; DB 6; Length 1002;
Best Local Similarity 75.4%; Pred. No. 4e-136;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACATATGGAGCTGAGTACACTCTCTGTGATGGCCCTCTGCTCTGTGTTCTT 76
DB 20 GCACATATGGAGCTGAGTACACTCTCTGTGATGGCCCTCTGCTCTGTGTTCTT 76
QY 77 CCATGAAGATCAAGCATATTTCAACAAGACTGGAACTGCCATTTTACAAACT 136
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DB 140 CTCAAAACCAAGCTGAGTACAGTCTGATGATTTTGGCAGAGCAAGATTAAGCTGTTG 199
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DB 320 AGGGCTTATCATGATGATTCATTCATCAACAAAGCCACAGGAATGTTGGCATCCACC 379
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QY 437 CTATATGAAGCAAGAAATTTCTGGCATTCATTAATTTGACCTGCTCATCTATACAGGTTACC 496
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LOCUS	ARI47736	1002 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 33 from patent US 6225042.		
ACCESSION	ARI47736		
VERSION	ARI47736.1 GI:15111826		
KEYWORDS	.		
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	1 (bases 1 to 1002)		
AUTHORS	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.		
TITLE	Antigen presenting system and methods for activation of T-cells		
JOURNAL	Patent: US 6225042-A 33 01-MAY-2001;		
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Query Match	54.28;	Score 540;	DB 6;	Length 1002;
Best Local Similarity	75.48;	Pred. No. 4e-136;		
Matches 743;	Conservative	0;	Mismatches 225;	Indels 18;
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Best Local Similarity 75.7%; Pred. No. 1.1e-139;
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RESULT 11
AX188198
LOCUS AX188198 Sequence 3893 from Patent WO012467.
DEFINITION AX188198
ACCESSION AX188198
VERSION AX188198.1 GI:15139671
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2205)
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 012467-A 3893 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
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BASE COUNT 650 a 477 c 466 g 610 t 2 others
ORIGIN

Query Match 55.5%; Score 553; DB 6; Length 2205;
Best Local Similarity 75.7%; Pred. No. 1.1e-139;
Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
QY 4 GGCATTGTGACAGACATATGGGACTGATGACACTCTCTTGTGATGGCCCTCTGCTC 63
Db 171 GGCATTGTGACAGACATATGGGACTGATGACACTCTCTTGTGATGGCCCTCTGCTC 230
QY 64 TCTGCTGTTCTTCATGAGATTCAGATATTTCAACAAGACTGGAACCTGCAATGC 123
Db 231 TCTGCTGCTGCTCTGAGATTCAGATTAATTTCAATGAGACTGCAAGCTGCAATGC 290
QY 124 CATTTTCAAACTCTCAAAACATAAGCTGATGAGCTGATATTTTGGCAGAGAC 183
Db 291 CAATTTGCAAACTCTCAAAACCAAGCTGATGAGCTAGTATTTTGGCAGAGAC 350
QY 184 GATAGCTGCTTCTGATGAGATTAATTCAGAGGCAAGAAAGCAACCTCAAAATGCTATC 243
Db 351 GAAACTTGTGCTGATGAGATTAATTCAGAGGCAAGAAATTTGACAGGTTCAATTC 410
QY 244 AAATTAAGGCGCTTACAGCTTTGACAGCAAGCAAGCTGAGACTCCAAATGTT 303
Db 411 AAGTATATAGGCGCGACAAAGTTTATTCGAGACGTTGAGACCTTGACACTTCAAACT 470

QY 958 TTGAAGACAGCCTCAGCGACAAAAGTACTACATTTT 996
 Db 1078 TCGAAGACATCTTCATCGCACAAAAGTATACATGTTTT 1116

RESULT 9
 AX332506 1424 bp DNA linear PAT 09-JAN-2002
 LOCUS Sequence 3015 from Patent WO0194629.
 DEFINITION AX332506
 ACCESSION AX332506
 VERSION AX332506.1 GI:18123140
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets

TITLE
 Patent: WO 0194629-A 3015 13-DEC-2001;

JOURNAL
 Avalon Pharmaceuticals (US)

FEATURES
 source
 1..1424
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 429 a 306 c 284 g 405 t

ORIGIN

Query Match 55.58; Score 553; DB 6; Length 1424;
 Best Local Similarly 75.7%; Pred. No. 1..1e-139;
 Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

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QY 64 TCTGTGTTCTTCATGACAGTCAAGCATATTTCAACAAAGCTGGAATGCCATGC 123
 Db 190 TCTGTGTTCTTCATGACAGTCAAGCATATTTCAACAAAGCTGGAATGCCATGC 249

QY 124 CATTTTCAAACTCTCAAAACATAGGCTGGATGAGCTGTGATATTTGGCAGACAG 183
 Db 250 CAATTTGAAACTCTCAAAACATAGGCTGGATGAGCTGTGATATTTGGCAGACAG 309

QY 184 GATAAGCGGTTCTGTATGATATTCAGAGGCAAGAAAGCAACCTCAAAATGTTTCATCTC 243
 Db 310 GATAAGCGGTTCTGTATGATATTCAGAGGCAAGAAAGCAACCTCAAAATGTTTCATCTC 369

QY 244 AAATATTAAGGCGGTACAGCTTTGACAGAGCAACTGGACCTGAGACTCCACATATGTT 303
 Db 370 AAATATTAAGGCGGTACAGCTTTGACAGAGCAACTGGACCTGAGACTCCACATATGTT 429

QY 304 CAGATCAAGGCAAGGAGCATATCAGTGTTCATTCATTAATAAGGCGCAAGAGCTA 363
 Db 430 CAGATCAAGGCAAGGAGCATATCAGTGTTCATTCATTAATAAGGCGCAAGAGCTA 489

QY 364 GTTCCCATGACCAAAATGAGTTCTGACCTATCATGCTTGTGTAATTCAGTCAACCTGAA 423
 Db 490 GTTCCCATGACCAAAATGAGTTCTGACCTATCATGCTTGTGTAATTCAGTCAACCTGAA 549

QY 424 ATACAGTAACTTCTATATGACAGAAAATTTCTGGCATCATAAATTTGACCTGCTATCT 483
 Db 550 ATACAGTAACTTCTATATGACAGAAAATTTCTGGCATCATAAATTTGACCTGCTATCT 606

QY 484 ATACAGTAACTTCTATATGACAGAAAATTTCTGGCATCATAAATTTGACCTGCTATCT 543
 Db 607 ATACAGTAACTTCTATATGACAGAAAATTTCTGGCATCATAAATTTGACCTGCTATCT 666

QY 544 ACTAAGTATGATCTGTATGAGAAATCTCAAAATATATGACAGAACTGTACACGTT 603

Db 667 ATCGATATGATGATATATGACAGAAATTCAGATTAATGTACAGAACTGTACAGCTT 726
 QY 604 TCTATCAGCTTCTCTTTTTCAGTCCCTGAG---CACAAATGTAGAGGCTTTTGTC 660
 Db 727 TCCATCAGCTTCTCTTTTTCAGTCCCTGAG---CACAAATGTAGAGGCTTTTGTC 786

QY 661 CTGAACCTGACAGCACTGGAGATGCTCTCTCCATCTTCAATATGATGACAACT 720
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QY 721 AAGCATTAAGACCTGACAGCACTGGAGATGCTCTCTCCATCTTCAATATGATGACAACT 780
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QY 781 GTTGTCTTTTGTGGGATGCTCTCTTAAACACTTAAGAAAGAGAGAGAGAGAGCT 840
 Db 898 ATTATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957

QY 841 GGCCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 958 GGCCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017

QY 901 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 Db 1018 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077

QY 958 TTGAAGACAGCCTCAGCGACAAAAGTACTACATTTT 996
 Db 1078 TCGAAGACATCTTCATCGCACAAAAGTATACATGTTTT 1116

RESULT 10
 HS004343 1424 bp mRNA linear PRI 15-JUL-1996
 LOCUS HS004343
 DEFINITION Human CD86 antigen mRNA, complete cds.
 ACCESSION U04343
 VERSION U04343.1 GI:439838
 KEYWORDS B70; B7-2.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 1424)
 Azuma, M., Ito, D., Yagita, H., Okumura, K., Phillips, J.H., Lanier, L.L.
 and Somoza, C.
 B70 antigen is a second ligand for CTLA-4 and CD28

JOURNAL
 Nature 366 (6450), 76-79 (1993)
 MEDLINE
 94050123
 2 (bases 1 to 1424)
 Fernandez-Ruiz, E., Somoza, C., Sanchez-Madrid, F., and Lanier, L.L.
 same region as CD80 (B7/B7.1) gene in human chromosome 3q13-q23

REFERENCE
 1 (bases 1 to 1424)
 Unpublished
 Somoza, C.

JOURNAL
 Direct Submission
 Submitted (14-DEC-1993) Chomorro Somoza, Human Immunology, DNAX
 Research Institute of Molecular and Cellular Biology, 901
 California Avenue, Palo Alto, CA 94304, USA

TITLE
 Submitted (14-DEC-1993) Chomorro Somoza, Human Immunology, DNAX
 Research Institute of Molecular and Cellular Biology, 901
 California Avenue, Palo Alto, CA 94304, USA

FEATURES
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 /chromosome="3"
 /map="3q13-q23"
 /cell_line="JY EBV B lymphoblastoid line"
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 148..1119
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 /note="common synonyms are B7-2 and B70; B70 antigen;

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Db	20	GCATATGGGAGCTAGTACACTCTCTCTGATGAGCCCTCTGCTCTGCTGTTTCTT	79	
QY	77	CCATGAAGAGTCAAGCATATTTCAACAAGAGCTGGAGACTGCCATGCTTTCAAACT	136	
Db	80	CCATGAAGAGTCAAGCATATTTCAACAAGAGCTGGAGACTGCCATGCTTTCAAACT	139	
QY	137	CTCAAAACATTAAGCTGGATGAGTGTATTTTGGCAGAGCCAGATTAAGCTGTTT	196	
Db	140	CTCAAAACATTAAGCTGGATGAGTGTATTTTGGCAGAGCCAGATTAAGCTGTTT	199	
QY	197	TGTATGAGATATTCAGAGGCAAGAGACCCGCAAAATGTTTCATCTCAATATAGGCC	256	
Db	200	TGTATGAGATATTCAGAGGCAAGAGACCCGCAAAATGTTTCATCTCAATATAGGCC	259	
QY	257	GTACAAGCTTTGACAAGGACAAGTGGACCTGAGACTCCACATGTTTCAGATCAAGACA	316	
Db	260	GCACAAGCTTTGACAAGGACAAGTGGACCTGAGACTCCACATGTTTCAGATCAAGACA	319	
QY	317	AGGGCACATATCTCACTGTTTCATTCATTAATAAGGCCCAAGAGACTAGTCCATGAC	376	
Db	320	AGGGCTTTGATTCATATGTTTCGTTTCATCAATAAGGGCCCAAGAGACTGTTCCATGAC	379	
QY	377	AAATGAGTGTCTGACCTATCAGTGTGCTGCTACCTGAGTCAAGTCAAGTCAAGTCAACT	436	
Db	380	AGATGATTTCTGACCTATCATGCT		

source		1. 1424	/organism="Homo sapiens"		
BASE COUNT		429 a	/db_xref="taxon:9606"		
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Query Match		55.5%;	Score 553;	DB 6;	Length 1424;
Best Local Similarity		75.7%;	Pred. No. 1.1e-139;		
Matches 756;		Conservative	0;	Mismatches 225;	Indels 18; Gaps 5;
QY	4	GGCATTTGTACACAGTATGAGTGAAGTCAAGTCTCTGTTGATGGCCCTGCTC	63		
Db	130	GGCATTTGTACACAGTATGAGTGAAGTCAAGTCTCTGTTGATGGCCCTGCTC	189		
QY	64	TCTGGTCTCTCCCTGGAAGATTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	123		
Db	190	TCTGGTCTCTCCCTGGAAGATTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	249		
QY	124	CATTTCACAACCTCTCAAAACATTAAGCTGATGAGTCAAGTCAAGTCAAGTCAAG	183		
Db	250	CAATTTCACAACCTCTCAAAACATTAAGCTGATGAGTCAAGTCAAGTCAAGTCAAG	309		
QY	184	GATAGCTGTTTGTATGATATTCAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG	243		
Db	310	GAAAGCTTGGTCTGATGATGAGTATTCAGAGCAAGAGAGAGAGAGAGAGAGAGAG	369		
QY	244	AAATATPAGGGCGGTCAACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG	303		
Db	370	AAATATPAGGGCGGTCAACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG	429		
QY	304	CAGATCAAG	363		
Db	430	CAGATCAAG	489		
QY	364	GTTCCCATGAGCAAAATGAGTGTGACATATGAGTGTGCTGCTGCTGCTGCTGCTG	423		
Db	490	ATTGAGATCCACGAGATGATTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	549		
QY	424	ATACAGTAACTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	483		
Db	550	ATACAGTAACTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	606		
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Db	607	ATACAGTAACTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	666		
QY	544	ACTAATGATGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	603		
Db	667	ATGAGATGATGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	726		
QY	604	TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660		
Db	727	TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	786		
QY	661	CTGAAATGAG	720		
Db	787	CTGAAATGAG	837		
QY	721	AAGGATTAAG	780		
Db	838	GAGGAG	897		
QY	781	GTTGTTTGTGAGATGATGCTGCTTAAACATTAAGAGAGAGAGAGAGAGAGAGAGAG	840		
Db	898	ATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	957		
QY	841	GGCCCTCTCATGAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	900		
Db	958	CGCACTCTTAATAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1017		
QY	901	GAAAGATTAAG	957		
Db	1018	AAAAG	1077		

[illegible]

Query Match	62.5%:	Score 622.8:	DB 6:	Length 994:
Best Local Similarity	80.7%:	Pred. No. 1.2e-158:		
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QY	22	ATGGAGCTGAGTACACACTCTCCCTTGTTGATGGCCCTCCGCTCTCGTGGTTTCTTCCATG	81	
Db	1	ATGGAGCTGAGTAAACATCTCTTGTGTGATGGCTCCGCTCCGCTCGTGGTGGCTCCCTTG	60	
QY	82	AAGACTCAAGCATTTTCAACAAGCTGGAGAAAGCCATGGCATTTTACAAGCTGCA	141	
Db	61	AAAATCTCAGGCAATTTTCAATGAGACTGGAGAACTGGCCGTGCATTTTACAAGCTGGAG	120	
QY	142	AACATAAGCCCTGATGAGCTGGTACTATTTTTGGCAGGACAGATTAAGCTGGTCTGTAT	201	
Db	121	AACCTAAGCCTGATGAGCTGGTACTATTTTTGGCAGGACAGATTAAGCTGGTCTGTAC	180	
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Db	181	GAGCTATATCCCGGACCAAGAGAGAGGCTCATATATGTTAAATTCGAAGTATATGGGTCCACA	240	
QY	262	AGCTTTGACAAGGACAACGTGAGACCCCTGAGACTCCACAATGTTCCAGATCAAGGACAAGGGC	321	
Db	241	AGCTTTGAACAGGGCACCGACCGCTGAGACTCCACAAGTTCAATCAAGGACAAGGGC	300	
QY	322	ACATATCACTGTTTATTCATTATTAAGGGCCCAAGGACATGTTCCCTGCACCAATAG	381	
Db	301	TCAATATCAATGTTTATTCATCCATCATTAAGGGCCGCACTGGCTGTTCTATCCACCAAGAG	360	
QY	382	AGTTTGTGACCTATCAGTGGTCTGTCACTCACTCACTCAACCGAATATACATCACTTCTAAT	441	
Db	361	AGTTTGTGACCTATCAATGGTCTGTCACTCACTCACTCAACCGAATATACATCACTTCTAAT	420	
QY	442	AGACACAGAAATTCGTGGCATCAATAATTTGACCTGCTCAATATACAGAGTTACCCAGAA	501	
Db	421	CACACAGAAATTTCTG---TCATTAATTTGACCTGCTCACTCAACACAGGTAACCCAGAA	477	
QY	502	CCTAAGGAGATGTATTTTTCAGCTAAACACTGGAATTCACATCACTAAGTATGATCTGAC	561	
Db	478	CCCCAGAGATGTATATGTGCTAAATACGAAATTCACACCATCAGCATGATGCTGAC	537	
QY	562	ATGAGAAATTCGAAATATATGTCAGACACTGTACACAGTTTCTATCAGCTTGCCTTTT	621	
Db	538	ATGAGAAATTCGAAATATATGTCAGACACTGTACACAGTTTCTATCAGCTTGCCTTTT	597	
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Db	598	CCCATCCCTCCGAGACAAATGAGACATGCTGTGTGCTCTGCACATTTGAGCCACAGCAAG	657	
QY	682	A---TGCTGCTCTCCCTACCTTTCATATATAGATGCACAACCTTAAGCATTAAGACCCCTGAA	738	

Db	658	ACACTGCTTTCTCCCTACCTCTGTAATATACATGGAAGGCCACCGTGCACACCCCTGTC	717
QY	739	CAAGGCCACTTTCCTCGATTGCGGCTGTACTGTAACTGTTGTTGTTTTGGGATG	798
Db	718	CCAGACCACATCTCCTGTGATTGACGCTCTACTGTAAACAGTGTCGTGTGTGTGGATG	777
QY	799	GTGTCTTTTAAACACTAAGGAAAAAGAAAGAACGACCTGGCCCTGCATGAAT--	856
Db	778	GTGTCTTTTGTAACTTAAGGAAAAAGAAAGAACGACCTGGCCCTGTAAATGAATGT	837
QY	857	-GTGAACCATCAAAAGGAGAGAAAAAGACAGACCAACGAAAGATACCATAC	915
Db	838	GCTGAACCATCAAAATATATAACAGGAAGCGAGCTGAACCAACTAACAACAGAGCA-----	891
QY	916	CACGTACCTGAGAGATCTGATGAAGCCCAAGT--TATTACATTTTGAAGACAGCTCA	972
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RESULT 7				
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DEFINITION	Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.			
ACCESSION	AF106827			
VERSION	AF106827.1	GI:6572518		
KEYWORDS				
SOURCE	dog.			
ORGANISM	Canis familiaris			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
AUTHORS	1 (bases 1 to 1795)			
TITLE	Yang, S., and Sim, G.-K.			
JOURNAL	New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules			
MEDLINE	Immunogenetics 50 (5-6), 349-353 (1999)			
REFERENCE	20093996			
AUTHORS	2 (bases 1 to 1795)			
TITLE	Yang, S., and Sim, G.-K.			
JOURNAL	Direct Submission			
FEATURES	Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA			
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ORIGIN				

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QY	797	TGCTGTCTTTTAAACACTAAGGAAAGGAGAAGAGCAGCCTGCCCCCTTCATGAAAT	856
Db	793	TGCTGTCTTTTAAACACTAAGGAAAGGAGAAGAGCAGCCTGCCCCCTTCATGAAAT	852
QY	857	GTGAAACCACTCAAAAGGGGAGAGAAAGAGAGCAAGCAGCAACGAAAGATACATACC	916
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QY	917	ACGTAAGTGAAGATCTGATGGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGGCG	976
Db	913	ATGGAACGGAAGATCTGATGGAAGCCCACTGATTAACATTTTGAAGACAGCCTCAGGCG	972
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Db	973	ACAAAGTACTACACATTTT 992	
RESULT 5			
LOCUS	PIGCDB6G	994 bp	linear
DEFINITION	Sus scrofa CD86 mRNA, complete cds.		
ACCESSION	L76099		
VERSION	L76099.1		
KEYWORDS	T cell costimulation.		
SOURCE	p1g.		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
AUTHORS	Maier,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and Botwell,A.L.		
TITLE	Porcine endothelial CD86 is a major costimulator of xenogeneic human T cells: cloning, sequencing, and functional expression in human endothelial cells		
JOURNAL	J. Immunol. 157 (9), 3838-3844 (1996)		
MEDLINE	97047772		
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Best Local	Similarity	80.7%	Pred. No. 1,2e-158:		
Matches 794:	Conservative	0:	Mismatches 172:	Indels 18:	Gaps 5
QY	22	ATGGAGCTGAGTCACACTCTCTCTTGTGATGGCCCTCTCTCTGTGTCTTCCATG	81		
Db	1	ATGGGACTGATACATCTCTTGTGTGATGTCTCTCTCTCTGTGTCTCTCTG	60		
QY	82	AAGAGTCAGGCAATATTTCAACAAGACTGGAGAATGCCATGGCATTTTTCAAACTCTCA	141		
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QY	442	AGAAGAGAAATTTGGGATCATTAATTTGACCTGCTCATCTATACAGGTTTACCAGAA	501		
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QY	502	CCTAAGGAGATTTTTCAGCTTAACACTGAGATTTCAACTACTAATGATGATCTGTC	561		
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QY	562	ATGAAGAAATCTCAAAATTAATGTGACAGAACTGATCAACGTTTCTATCAAGCTTGTCT	621		
Db	538	ATGAAGAAATCTCAAAATTAATGATCAACGAGACTCTCAATGATATCAATCAGGGTGTCTT	597		
QY	622	TCAGTCCTGGAAGCACACATGTGAGCGTCTTTTGGCCCTGAACCTGAGACACTGAG	681		
Db	598	CCCATCTCCCGAGACAATTTGTGACATGCTGTCTCTGACCACTTGAGCACAAG	657		
QY	682	A -- TGCTGCTCTCCCTCACTTCAATTAATGATGACACAACCTAAGGATTAAGACCTGAA	738		
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QY	739	CAGGCACTTCTCTGATTTGCGGCTGCTACTTGTAAATGTTTGTGTTTGTGGATG	798		
Db	718	CCAGACCACTCTCTGATTTGCACTCTACTTGTAAACAGTGTGTGTGTGGATG	777		
QY	799	GTCGCTTTTAAACACTTAAGGAAAGAAAGAAAGACGCTGGCCCTCTCATGAT --	856		
Db	778	GTCGCTTTTAAACACTTAAGGAAAGAAAGAAAGACGCTGGCCCTCTCATGAT	837		
QY	857	GTGAACCACTCAAAAGGAGAAAGAAAGAAAGACCAACGACCAAGAAAGATACATAC	915		
Db	838	GSTGAACCACTCAAAATTAACAGGAAGGCGATGACCAACTAAGACACAGCA -----	891		
QY	916	CACGTACTGAGAGATCTGATGAAGCCCAAGT -- TATTAATTTTGAAGACAGACCTCA	972		
Db	892	GAACTCATGAGACATCTGATGATGCCCAAGTGTATTTTAAAGACAGCTCA	951		
QY	973	GCGCAAAAGTACTACATTTT 996			
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CDS						
3' UTR	966. 1897					
BASE COUNT	585 a	400 c	383 g	529 t		
ORIGIN						
Query Match	78.8%;	Score 784.8;	DB 4;	Length 1897;		
Best Local Similarity	89.08;	Pred. No. 9.3e-203;				
Matches 872;	Conservative	0;	Mismatches 102;	Indels 6;	Gaps 2;	
17	GCACATGAGCACTGAGTCACACCTCTCTTGTGATGAGCCCTCGTCTCTGTTCTT	76				
19	GCACATGAGCACTGATTAACATCTCTTGTGATGAGCCCTCGTCTGATGAGTCT	78				
77	CCATGAGAGTCACGATATTTTCAACAAGCTGGAGAACCTGCATGCCATTTACAACT	136				
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Query Match 99.8%; Score 994.4; DB 4; Length 1270;
Best Local Similarity 99.9%; Pred. No. 8.5e-260;
Matches 995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
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LOCUS AF157827
DEFINITION Felis catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
ORGANISM
cat.
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 (bases 1 to 1138)
AUTHORS Choi,I.S., Hash,S.M., Winslow,B.J. and Collisson,E.W.
TITLE Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
PUBMED 10713336
REFERENCE
2 (bases 1 to 1138)
AUTHORS Choi,I.S., Hash,S., Winslow,B.J. and Collisson,E.W.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA
FEATURES
location/Qualifiers
source 1..1138
/organism="Felis catus"
/db_xref="taxon:9685"
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gene /gene="CD86"
63..1052
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BASE COUNT 358 a 245 c 246 g 289 t
ORIGIN
Query Match 98.5%; Score 980.8; DB 4; Length 1138;
Best Local Similarity 99.8%; Pred. No. 4.3e-256;
Matches 982; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 1363.8 Seconds
(without alignments)
15282.914 Million cell updates/sec

Title: US-09-646-561-28

Perfect score: 996
Sequence: 1 atgggcatctgtacagcac.....acaaagtactacacattt 996

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
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29: em_vi:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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2	994.4	99.8	1270	4	AB030652	AB030652 Felis cat
3	980.8	98.5	1138	4	AF157827	AF157827 Felis cat
4	784.8	78.8	1897	4	AF106826	AF106826 Canis fam
5	622.8	62.5	994	4	PICD86C	L76099 Sus scrofa
6	622.8	62.5	994	6	AX027016	AX027016 Sequence
7	582.2	58.5	1795	4	AF106827	AF106827 Canis fam
8	553	55.5	1424	6	AX330924	AX330924 Sequence
9	553	55.5	1424	6	AX332506	AX332506 Sequence
10	553	55.5	1424	6	HSU04343	U04343 Human CD86
11	553	55.5	2205	6	AX188198	AX188198 Sequence
12	540	54.2	1002	6	AR147736	AR147736 Sequence
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14	540	54.2	1002	6	AR160450	AR160450 Sequence
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17	540	54.2	1120	6	AR112747	AR112747 Sequence
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34	330	33.1	1261	6	AR146408	AR146408 Sequence
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ALIGNMENTS

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DEFINITION AY007704
ACCESSION AY007704 GI:15418725
VERSION
KEYWORDS
SOURCE
ORGANISM

cat.
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 (bases 1 to 2830)
AUTHORS Yang,S., Sellins,K.S., Powell,T., Stoneman,E. and Sim,G.K.
TITLE Novel transcripts encoding secreted forms of feline CD80 and CD86
JOURNAL Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)
MEDLINE 21390213
PUBMED 11498243
REFERENCE 2 (bases 1 to 2830)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA

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Db 508 ATTGCGATCCACGATGATTTCTGACCTGTCAGTGGTTCGTAACCTCAGTCAACCTGAA 567
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Search completed: October 19, 2002, 23:35:47
Job time : 36.1303 secs

Query Match	55.2%	Score 463.8	DB 5	Length 1120
Best Local Similarity	80.5%	Pred. No. 7.7e-136		
Matches 569	Conservative 0	Mismatches 132	Indels 6	Gaps 2

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US-08-205-697A-24

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Best Local Similarity	80.5%;	Pred. No. 7.9e-136;		
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: APPLICATION NUMBER: US 08/205,697
: FILING DATE: 02-Mar-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragouras, Amy E.
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: BMI-120CPUS
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 107..1093
: US-08-702-525-22
:
Query Match 55.2%; Score 463.8; DB 4; Length 1120;
Best Local Similarity 80.5%; Pled No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2
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; STATE: Massachusetts
; COUNTRY: USA
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPT-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-280-757B-1

Query Match          55.2%; Score 463.8; DB 3; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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Db      584 ATACAGGTTACCCAGAGAGATGATTTTGTGTAATAAACCGAATTCAGT 643
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Db      704 TCCATCAGCTTGTCTGTTTCATTCCTGATGTATACGAGCAATATGACCATCTTCTGATTT 763
Qy      658 CTCGACTTGAATCAATGAGCTTCCTCCCTCACTTATATATATAGA 704
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      764 CTGAAACTGACAGACCGCGCTTTATCTTCACCTTCTCTATAGA 810

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RESULT 11
US-08-205-697A-22
; Sequence 22, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Boriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510e1 Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMT-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-205-697A-22

Query Match          55.2%; Score 463.8; DB 4; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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Db 467 ATTGCATCCACCAGATGAATTCGTGACGTGCTGCTGCTAATCTCAGTCAACCTGAA 526
Qy 421 ATATGTACTTCTATATAGAACAGAAATTCGCGCATCAATATTTGACCTGCTCATCC 480
Db 527 ATAGTACCAATTTCTATATTAACAGAAA---TGTCTACATATAATTTGACCTGCTCATCT 583
Qy 481 ATACAGGTTTACCCAGAACCCAGAGATGATTTTGGTAAACCGAGAAATTCAGT 540
Db 584 ATACAGGTTTACCCAGAACCCAGAGATGATTTTGGTAAACCGAGAAATTCAGT 643
Qy 541 ACTAATGATGATCTGTCATGGAAGAAATCTCAAAATTAATGTACAGACTCTACACGTT 600
Db 644 ATCGATATGATGATGATTTATTCAGAAATCTCAAGATTAATGTACAGACTGTACAGCGTT 703
Qy 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTCTC 657
Db 704 TCCATCAGCTTGTCTCTCTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTCTC 763
Qy 658 CTGCAACTTGAGTCAATGAAGCTTCCCTCCCTACCTTATATATATAGA 704
Db 764 CTGGAACCTGACAGACGCGCTTTATCTTCACTTCTCTATATAGA 810
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RESULT 9

US-08-479-744A-1

Sequence 1, Application US/08479744A

Patent No. 6084067

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,744A

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/280,757

FILING DATE: 26-JUL-1994

APPLICATION NUMBER: 08/109,393

FILING DATE: 28-AUG-1993

APPLICATION NUMBER: 08/101,624

FILING DATE: 26-JULY-1993

APPLICATION NUMBER: 08/147,773

FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-004CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1120 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

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FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-479-744A-1
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Query Match 55.2% Score 463.8; DB 3; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;
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Qy 1 ATGTATCTCAATGACATATGAACTGATTAACATTTCTTTTGATGACCTCTGCTC 60
Db 107 ATGATCCCCAGTCCACATATGAGGACTGATGAACATTTCTTTTGATGAGGCTTCTGCTC 166
Qy 61 TATGATGCTGCTTCCATGAGAGTCAAGATATTTCAACAAAGATGAGCAAGTCCATGTC 120
Db 167 TCTGTGCTGCTCTCTCTGATGATTTCAAGCTTATTTCAATGAGACTGACAGCTGCTCATGTC 226
Qy 121 CATTTTCAAAATTTCTCAAAACATTAAGCTTGATGATGTTGATGTTTGGCAGGACAG 180
Db 227 CAATTTGCAAACTCTCAAAACCAAAAGCTGATGAGCTAGTATTTTGGCAGGACAG 286
Qy 181 GATAAGCTGTTCTGTACGACTATACAGAGGCAAGAACCTCAAAATTTTCATGCG 240
Db 287 GAAACCTGTTCTGATGATGAGTATCTTACGCAAGAAATTTGACAGTTCATTTCC 346
Qy 241 AAGTATAAGGCGCCGACAGCTTTGACAAAGACATTTGACACCTGACAGCTCCATTAATTT 300
Db 347 AAGTATATGAGGCGCCGACAGCTTTGATTTGATTTGACAGCTTTGACAGCTTTCAACATTT 406
Qy 301 CAGATCAAGGACAAAGGCTTTGATCAATGTTTCTGATCATTAAGGCGCCCAAGGACATC 360
Db 407 CAGATCAAGGACAAAGGCTTTGATCAATGTTTCTGATCATTAAGGCGCCCAAGGACATC 466
Qy 361 GTTCCATGCAACGAGATGATTTGACCTATACAGTGTCTGCTCACTTCACTCAACCTGAA 420
Db 467 ATTCGATCCACGACGATGATTTGACAGTGTCTGCTCACTTCACTCAACCTGAA 526
Qy 421 ATATGTACTTCTATATAGAACAGAAATTCGCGCATCAATATTTGACCTGCTCATCC 480
Db 527 ATAGTACCAATTTCTATATTAACAGAAA---TGTGTACATATAATTTGACCTGCTCATCT 583
Qy 481 ATACAGGTTTACCCAGAACCCAGAGATGATTTTGGTAAACCGAGAAATTCAGT 540
Db 584 ATACAGGTTTACCCAGAACCCAGAGATGATTTTGGTAAACCGAGAAATTCAGT 643
Qy 541 ACTAATGATGATCTGTCATGGAAGAAATCTCAAAATTAATGTACAGACTCTACACGTT 600
Db 644 ATCGATATGATGATGATTTATTCAGAAATCTCAAGATTAATGTACAGACTGTACAGCGTT 703
Qy 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTCTC 657
Db 704 TCCATCAGCTTGTCTCTCTCTCAGTCCCTGAAG---CAAGCAATGTGAGCATCTTCTGTCTC 763
Qy 658 CTGCAACTTGAGTCAATGAAGCTTCCCTCCCTACCTTATATATATAGA 704
Db 764 CTGGAACCTGACAGACGCGCTTTATCTTCACTTCTCTATATAGA 810
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RESULT 10

US-08-280-757B-1

Sequence 1, Application US/08280757B

Patent No. 6130316

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-456-104-1

Query Match 55.2%; Score 463.8; DB 2; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 369; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTATCTCAGATGACATATGAACTGAATTAACATTCCTCTTGTGATGACCTCTGCTC 60
DB 107 ATGATGCCCACTGACATATGAGACTGAGTAACATTCCTCTTGTGATGACCTCTGCTC 166
QY 61 TATGTCCTCTTCATGAGAGTCAAGCATATTTCAACAAGCTGGAGACTGCCATGC 120
DB 167 TCTGTGCTCTCTCTCTGAGATTCAAGCTTATTTCAATGAGACTGACAGCCTGCATGC 226
QY 121 CATTTCACAAATTCCTCAAAACATTAAGCCTGATGAGTGTGATGTTTGGCAGACAG 180
DB 227 CAATTTCCAAACTCTCAAAACCAAGCCTGATGAGTGTGATGTTTGGCAGACAG 286
QY 181 GATAAGCTGTCTGTGAGAGCTATACAGAGGCAAGAACCCCTCAAAATGTTCAATCGC 240
DB 287 GAAACTGTTGCTGATGATGAGTATCTACTGAGCAAGAAATTTGACAGTGTTCATTC 346
QY 241 AAGTATGAGGGCGCAACCTTGCACAAAGCAATTTGACCTGAGACTGCATATATT 300
DB 347 AAGTATGAGGGCGCAACCTTGTGATGCGACAGTTGGACCTGAGACTGCATATATT 406
QY 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGCTTCATCATTAAGGCGCCCAAGAGACTC 360
DB 407 CAGATCAAGGACAAAGGCTGTATCAATGTTGCTTCATCATCAACAAAGCCACAGAGATG 466
QY 361 GTTCCCATGACCAAGATGATTTCTGACCTATCAGCTGTTCTTAATTCACTCAACCTGAA 420
DB 467 ATTGCGATCCACAGAGATGATTTGAACTGTGACGTCTCACTCACTCAACCTGAA 526
QY 421 ATATGTTAATCTCTATATAGCAAGAAATTTGCGCATCATTAATTTGACCTGCTCATCC 480
DB 527 ATATGTTAATCTCTATATATACAGAAAA--TGTGACATTAATTTGACCTGCTCATCT 583
QY 481 ATACAGGTTACCCAGAACCCAGAGAGATGATTTTTTGGTAAAAACCGAAGATTCAGT 540
DB 584 ATACAGGTTACCCAGAACCCAGAGATGATGATGTTTGGTAAAGAACCAAGATTCAGT 643
QY 541 ACTAGATATGATCTGATGATGAGAAATCTCAAAATTAATGTCACAGACTCTCAACGTT 600
DB 644 ATCAGATATGATGATGATGATGAGCAAAATCTCAAGATTAATGTCACAGAGTACAGAGT 703
QY 601 TCTATCAGCTGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 657
DB 704 TCCATCAGCTGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 763
QY 658 CTGCACTGTGAGTCAATGAGCTTCCCTCCCTACCTTATATATATAGA 704
DB 764 CTGCACTGTGAGTCAATGAGCTTCTTATCTTCACTTCTCTATAGA 810

RESULT 8
US-08-101-624-1
Sequence 1, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTL44/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-101-624-1

Query Match 55.2%; Score 463.8; DB 2; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 369; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTATCTCAGATGACATATGAACTGAATTAACATTCCTCTTGTGATGACCTCTGCTC 60
DB 107 ATGATGCCCACTGACATATGAGACTGAGTAACATTCCTCTTGTGATGACCTCTGCTC 166
QY 61 TATGTCCTCTTCATGAGAGTCAAGCATATTTCAACAAGCTGGAGACTGCCATGC 120
DB 167 TCTGTGCTCTCTCTCTGAGATTCAAGCTTATTTCAATGAGACTGACAGCCTGCATGC 226
QY 121 CATTTCACAAATTCCTCAAAACATTAAGCCTGATGAGTGTGATGTTTGGCAGACAG 180
DB 227 CAATTTCCAAACTCTCAAAACCAAGCCTGATGAGTGTGATGTTTGGCAGACAG 286
QY 181 GATAAGCTGTCTGTGAGAGCTATACAGAGGCAAGAACCCCTCAAAATGTTCAATCGC 240
DB 287 GAAACTGTTGCTGATGATGAGTATCTACTGAGCAAGAAATTTGACAGTGTTCATTC 346
QY 241 AAGTATGAGGGCGCAACCTTGCACAAAGCAATTTGACCTGAGACTGCATATATT 300
DB 347 AAGTATGAGGGCGCAACCTTGTGATGCGACAGTTGGACCTGAGACTGCATATATT 406
QY 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGCTTCATCATTAAGGCGCCCAAGAGACTC 360
DB 407 CAGATCAAGGACAAAGGCTGTATCAATGTTATCATATCAACAAAGCCACAGAGATG 466
QY 361 GTTCCCATGACCAAGATGATTTCTGACCTATGAGTGTGATGATGATGATGATGATGATG 420

ANTI-SENSE: NO
US-09-039-982A-33

Query Match	55.28;	Score 463.8;	DB 4;	Length 1002;
Best Local Similarity	80.58;	Pred. No. 7.3e-136;		
Matches 569;	Conservative 0;	Mismatches 132;	Indels 6;	Gaps 2.

QY	1	ATGTAATCTCGAGATGCACTATGAGAACTGAATATACATTCCTCTTGTTGATGATGACCCCTCCGCTC	60
Db	7	ATGAGATCCCAAGTCACTATGAGGACGAGAACATTCCTCTTGATGATGGCTCCCTGCTC	66
QY	61	TATGCTGCTGCTTCATGAAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGGCATG	120
Db	67	TCTGTGCTGCTGCTCTCGAAGATTCAGAGCTATTTCAATAGACTGACAGCTGGCATG	126
QY	121	CATTTTCCAAATTTCTCAAAACATTAAGCGCTGGATGAGTTGGTATGTTTTGGCAGACAG	180
Db	127	CAATTTGCCAACTCTCAAAACCAAGCGCTGAGTGAAGTACTATATTTTGGCAGAACAG	186
QY	181	GATAAGCTGTTCTGTACGAGCTATACAGAGGCAAGAGAACCCCTCAAAATGTTCAATCCG	240
Db	187	GAAACCTGTTCTGTATGAGGTACTGTAGGCAAAAGAAATTTGCACTGTTCAATCC	246
QY	241	AAGATATAAGGGCCGACAAAGTTTGAACAAGCAATTTGSAACCGTGAGACTCCATATAT	300
Db	247	AAGTATATAGGGCCGACAAAGTTTGAATCGGACGTTTGGACCGTGAGACTTTCACAACTT	306
QY	301	CAGATCAAGGACCAAGGGCTGTATCAATGTTTTGTTCTTCATCAATAAAGGGCCCAAGGACTC	360
Db	307	CAGATCAAGGACCAAGGGCTGTATCATATGATCATCATCAACAAAAGCCCAAGGAAATG	366
QY	361	GTTCCCATGACCAAGATGATTTCTGACCTATCACTGCTTGCTTAATTCATTCACACTGAA	420
Db	367	ATTGCCATCCACAGATGTAATTTGAACTGTCACTGTTCTTAATTCATTCACACTGAA	426
QY	421	ATAATGGTAACCTTCATATAGAAACAGAAATTTCTGGCATCATAAATTTGACCTGCTCAATC	480
Db	427	ATAGTACCAATTTCTAATATATACAGAAAA---TGTGATCAATAATTTGACCTGCTCATCT	483
QY	481	ATACAGAGTTACCCAGAACCCAGAGAGATGTAATTTTTTGGTAATAAACCGAATTTCAAGT	540
Db	484	ATACAGAGTTACCCAGAACCTTAAGAGATGATGTTTTGGTATAGAACCAAGAAATTTCAACT	543
QY	541	ACTAGTATGATGATGTCATAGAGAAATCTCAAAATATATGTCACAGAACTCTCAACGTT	600
Db	544	ATCGAGTATGATGATATATATGTCAGAGAAATCTCAAAATATATGTCACAGAACTGTACGAGTT	603
QY	601	TCTATCACTGTCTCTTCTCACTGCTCTGAAG--CAAGCAATGTCAGCAATCTTGTGTCTC	657
Db	604	TCTATCACTGTCTCTTCTTCAATCTCCATGATGTACAGCAATATAGACCAATCTTGTATTT	663
QY	658	CTGCAACTTGATGATCAATGAAGTCTCCCTCACTTATATATATATAGA 704	
Db	664	CTGGAAGCTGCAAGACGGGGCTTTTATCTTCACCTTTCTCTATATAGA 710	

RESULT 5
 US-09-039-641-33
 ; Sequence 33, Application US/09039641
 ; Patent No. 6251627
 ; GENERAL INFORMATION:
 ; APPLICANT: Cai, Zeling
 ; APPLICANT: Sprent, Jonathan
 ; APPLICANT: Brunmark, Anders
 ; APPLICANT: Jackson, Michael
 ; APPLICANT: Peterson, Per A
 ; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
 ; TITLE OF INVENTION: ACTIVATION OF T-CELLS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Olsson & Hiertl, Ltd.
 ; STREET: 20 No. 6251627th Wacker Drive, Suite 3000
 ; CITY: Chicago

```

1 STATE: Illinois
2 COUNTRY: USA
3 ZIP: 60606
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patentn Release #1.0, Version #1.25
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/09/039,641
13 FILING DATE: 8-MAR-1995
14
15 CLASSIFICATION:
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Olson, Arne M.
18 REGISTRATION NUMBER: 30,203
19 REFERENCE/DOCKET NUMBER: TSRI4710
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (312) 580-1180
22 TELEFAX: (312) 580-1189
23
24 INFORMATION FOR SEQ ID NO: 33:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 1002 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: double
29 TOPOLOGY: linear
30
31 MOLECULE TYPE: cDNA
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34 HYPOTHETICAL: NO
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36 ANTI-SENSE: NO
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38 US-09-039-641-33
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 ; Search time 29.1303 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-19

Perfect score: 840

Sequence: 1 atgtatctcagatgcactat.....acaacagctactacagttt 840

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.8	55.2	751	4	US-09-039-982A-34 Sequence 34, Appl
2	463.8	55.2	751	4	US-09-039-641-34 Sequence 34, Appl
3	463.8	55.2	751	4	US-09-039-762A-34 Sequence 34, Appl
4	463.8	55.2	1002	4	US-09-039-982A-33 Sequence 33, Appl
5	463.8	55.2	1002	4	US-09-039-641-33 Sequence 33, Appl
6	463.8	55.2	1002	4	US-09-039-762A-33 Sequence 33, Appl
7	463.8	55.2	1120	2	US-08-456-104-1 Sequence 1, Appl
8	463.8	55.2	1120	2	US-08-101-624-1 Sequence 1, Appl
9	463.8	55.2	1120	3	US-08-479-744A-1 Sequence 1, Appl
10	463.8	55.2	1120	3	US-08-280-757B-1 Sequence 1, Appl
11	463.8	55.2	1120	4	US-08-205-697A-22 Sequence 22, Appl
12	463.8	55.2	1120	4	US-08-702-525-22 Sequence 22, Appl
13	463.8	55.2	1120	4	US-08-403-253A-3 Sequence 3, Appl
14	463.8	55.2	1120	5	PCT-US95-02576-22 Sequence 22, Appl
15	463.8	55.2	1161	4	US-08-205-697A-24 Sequence 24, Appl
16	463.8	55.2	1161	4	US-08-702-525-24 Sequence 24, Appl
17	463.8	55.2	1161	5	PCT-US95-02576-24 Sequence 24, Appl
18	463.8	54.6	1424	5	US-09-326-186B-226 Sequence 226, App
19	463.8	54.6	1428	5	PCT-US94-09642-1 Sequence 11, Appl
20	463.8	54.0	972	4	US-08-848-760B-11 Sequence 3, Appl
21	344.4	41.0	1151	2	US-08-456-104-3 Sequence 3, Appl
22	344.4	41.0	1151	4	US-08-205-697A-20 Sequence 20, Appl
23	344.4	41.0	1151	4	US-08-702-525-20 Sequence 20, Appl
24	344.4	41.0	1151	5	PCT-US95-02576-20 Sequence 20, Appl
25	344.4	41.0	1163	3	US-08-479-744A-22 Sequence 22, Appl
26	344.4	41.0	1163	3	US-08-280-757B-22 Sequence 22, Appl
27	337.2	40.1	1261	4	US-08-205-697A-12 Sequence 12, Appl

28	337.2	40.1	1261	4	US-08-702-525-12	Sequence 12, Appl
29	337.2	40.1	1261	5	PCT-US95-02576-12	Sequence 12, Appl
30	232.4	27.7	330	3	US-08-479-744A-44	Sequence 44, Appl
31	232.4	27.7	330	3	US-08-280-757B-46	Sequence 46, Appl
32	175.2	20.9	306	3	US-08-479-744A-46	Sequence 46, Appl
33	175.2	20.9	306	3	US-08-280-757B-46	Sequence 46, Appl
34	86.4	10.3	210	4	US-08-205-697A-31	Sequence 31, Appl
35	86.4	10.3	210	4	US-08-702-525-31	Sequence 31, Appl
36	86.4	10.3	210	5	PCT-US95-02576-31	Sequence 31, Appl
37	45	5.4	195	4	US-08-205-697A-41	Sequence 41, Appl
38	45	5.4	195	4	US-08-702-525-41	Sequence 41, Appl
39	45	5.4	195	5	PCT-US95-02576-41	Sequence 41, Appl
40	34.6	4.1	492	4	US-09-328-111-335	Sequence 35, App
41	33.4	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
42	33	3.9	2747	2	US-08-874-347-1	Sequence 1, Appl
43	33	3.9	2747	3	US-08-093-522-1	Sequence 1, Appl
44	32.4	3.9	3341	2	US-08-868-577-18	Sequence 18, Appl
45	32	3.8	3095	6	5231168-1	Patent No. 5231168

ALIGNMENTS

RESULT 1
US-09-039-982A-34
; Sequence 34, Application US/09039982A
; Patent No. 6225042
; GENERAL INFORMATION:
; APPLICANT: Cal, Zelig
; APPLICANT: Sprent, Jonathan
; APPLICANT: Brummark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6225042th Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,982A
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olson, Arne M.
; REGISTRATION NUMBER: 30,203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-039-982A-34

Query Match 55.2%; Score 463.8; DB 4; Length 751;
Best Local Similarity 80.5%; Pred. No. 6.3e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

PI	Slim G., Yang S., Sellins KS;
XX	WPI; 1999-571822/48.
XX	New Isolated B7 and CTLA4 nucleic acids, used to develop products for
PT	treating, e.g. autoimmune and atopic diseases -
XX	Claim 1; Page 121-123; 148pp; English.
PS	
XX	The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be
CC	expressed by standard recombinant methodology. The nucleic acid molecules
CC	and the encoded proteins can be used for preventing or treating diseases,
CC	e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC	development, graft rejection, inflammation, arthritic and atopic diseases
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC	cats, cattle, sheep or pets. The products can also be used for detection,
CC	diagnosis and drug screening.
XX	
SO	Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other:
	Query Match 69.3%; Score 582.2; DB 20; Length 2830;
	Best Local Similarity 89.4%; Pred. No. 1.2e-161;
	Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
OY	14 GCACCTATGAGACTGAATTAACTTTCTTTGTGTATGCACCCTCGCTCATGTGCTGCTT 73
Db	2636 GCACCTATGGACAGCACTCACAACCTCTCTGTGTATGGCCCTCGCTCTGTGGTTCCT 2577
OY	74 CCATGAGAAGTCAAGCATATTTTCAACAGACTGGAGAACCTGCCATGCCATTTACAAATT 133
Db	2576 CCATGAGAAGTCAAGCATATTTTCAACAGACTGGAGAACCTGCCATGCCATTTTACAACT 2517
OY	134 CTCAAACATAAGCCCTGGATGATGATGTTGTGTATGTTTTGGCAGGACCAAGATAAGCTGTTC 193
Db	2516 CTCAAACATAAGCCCTGGATGAGCTGTGTATGTTTTGGCAGGACCAAGATAAGCTGTTC 2457
OY	194 TGTAGAGCTATTAAGAGGCAAAAGAACCCCTCAAATTTTATGCGCAAGTATAAGGGCC 253
Db	2456 TGATATGATATTTCAAGAGCAAAAGAACCCCTCAAATTTTATCTCAATTTAAGGGCC 2397
OY	254 GCACAGCTTTTACAAGAGCAATTTGGACCTGAGACTCATTAATTTTGATCAAGAGACA 313
Db	2396 GTACAGCTTTTGAACAAGCAACTGGACCTGAGACTCACATTTTTCAGATCAAGAGACA 2337
OY	314 AGGCGTTGATCAATGTTTTCGTTCAATTAAGGCCCAAGAGACTCGTTCCATGCACC 373
Db	2336 AGGCGCATATTCAGTGTTCATTTAATAAAGGCCCAAGAGACTGATCCCATGCACC 2277
OY	374 AGATGATTTCTGACCATATAGTGCCTTGCACTTACCTGACCACTGAATTAATGTAACCT 433
Db	2276 AAATGATTTCTGACCTATCAGTGTCTTGCCTTAACCTTATAGTCACTGAATTAACAGTAACCT 2217
OY	434 GTAATAGAACAGAAAATCTGGCATCATTAATTTGACCTGTCATCCATCAAGGTTTACC 493
Db	2216 GTAATAGAACAGAAAATCTGGCATCATTAATTTGACCTGTCATCAAGGTTTACC 2157
OY	494 CAGAACCCAGAGAGATGATTTTTTGGTAAAAACCGAGAAATTCAGTACTAGTATGATA 553
Db	2156 CAGAACCTPAGAGATGATTTTTTGGTAAAAACCTGAGAAATTCAGTACTAGTATGATA 2097
OY	554 CGTGATATGAGAAATCTCAAAATATGTACAGAACTTACACAGTTCTCTACAGCTTGT 613
Db	2096 CGTGATATGAGAAATCTCAAAANTATGTGACAGAACTTACACAGTTCTCTACAGCTTGC 2037
OY	614 CCTTCVCACTCCCTGGAAGCAAGCAATGTGACATCTTGTGTCTGCAACTTATAGTCA 673
Db	2036 CTTTTCVCACTCCCTGGAAGCAACAATGTGAGCGCTTTTGTGSCCTGAACCTGAGACAC 1977
OY	674 T---GAACCTTCCTCCCTACCTTATATATAGAAACCAACAAAGTGAGAGAAA 725
Db	1976 TGGAACTCTCTCTCTCCCTACCTTTCATATATAGATGAGCAACCTTAGATTAAGAA 1922

PT Novel feline proteins used to produce feline vaccines which prevent
PT infectious disease or to promote growth in homologous or heterologous
PT species -

PS Claim 6; Fig 3A; 186pp; English.

CC This is the nucleotide sequence of cDNA encoding feline CD86
CC (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
CC peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
CC comprising nucleic acid encoding feline CD86 ligand or feline
CC soluble CD80 ligand is designated PSI-2#19-2/011298 (ATCC 209821).
CC The coexpression of CD86 with the costimulatory molecules CD28 (see
CC AAY32279) and a tumour antigen or an antigen from a pathogenic
CC organism has the ability to activate or enhance activation of
CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
CC the ability to regulate activation of T-lymphocytes. The invention
CC provides isolated nucleic acids encoding feline CD86 ligand,
CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
CC (CD152) receptor, as well as vectors comprising the nucleic acids,
CC and polypeptides encoded by the nucleic acids. It also provides
CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
CC further comprising immunogens derived from pathogens, especially
CC feline immunodeficiency virus (FIV), feline leukaemia virus,
CC feline infectious peritonitis virus, feline panleukopenia virus,
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
CC herpesvirus, feline Borna disease virus, rabies virus, chlamydia,
CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
CC pathogen, or parasite (all claimed). Vaccines capable of suppressing
CC an immune response (suitable for treating an autoimmune disease
CC or tissue or organ transplant rejection) are claimed. The
CC nucleic acids may be used for gene therapy or antisense therapy
CC protocols.

XX Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

Query Match 69.3%; Score 582.2; DB 21; Length 1080;
Best Local Similarity 89.4%; Pred. No. 7.5e-162;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 14 GCACATGGAACGTAATACATCTCTTTGTGATGACCCCTGCTATAGTGCCTT 73
DB 79 GCACTATGGAGCTGAGCACTCTCTCTGTGATGCGCCCTGCTCTGCGTTCCT 138
QY 74 CCATGAGAGCTCAAGCATATTTCAACAAGACTGAGAACTGCATGCCATTTCACAATT 133
DB 139 CCATGAGAGCTCAAGCATATTTCAACAAGACTGAGAACTGCATGCCATTTCACAAC 198
QY 134 CTCAAAACATPAGCCTGGATGAGTGTGCTGTTTGGCAGGACCAAGATPAGCTGTC 193
DB 199 CTCAAAACATPAGCCTGGATGAGTGTGCTGTTTGGCAGGACCAAGATPAGCTGTC 258
QY 194 TGTGAGAGCTATACAGGAGGCAAGAACCTCAAAATGTTCAATCCGAATATPAGGGCC 253
DB 259 TGTATGAGATATTTAGAGGCAAGAAAGAACCTCAAAATGTTCAATCTCAATATPAGGGCC 318
QY 254 GCACAGCTTTGACAAAGACATTTGACCCCTGAGACTCATATATTTTACAGTCAAGGACA 313
DB 319 GTACAGAGTTTGCACAAAGACAACTGAGACCTGAGACTCCACAANTGTTCAGATCAAGGACA 378
QY 314 AGGCTGTGATCAATGTTTCTGTTATCATATAAGGGCCCAAGAGACTGTTCCCATGACCC 373
DB 379 AGGCTGTGATCAATGTTTCTGTTATCATATAAGGGCCCAAGAGACTGTTCCCATGACCC 438
QY 374 AGATGAATTTGACATATCACTGCTGTGATCACTCAGTCAACCTGAATATATGATGACTT 433
DB 439 AATGAGTTTGCACATATCACTGCTGTGATCACTCAGTCAACCTGAATATATGATGACTT 498
QY 434 CTATATGAGACGAAATTTCTGATCATATTAATTTGACCTGCTCATATCAATCAAGGTTACC 493
DB 499 CTATATGAGACGAAATTTCTGATCATATTAATTTGACCTGCTCATATCAATCAAGGTTACC 558

QY 494 CAGAACCCAGAGATGATATTTTGGTAAACCCGAGAAATTCAGTACTAATGATGATA 553
DB 559 CAGAACCCAGAGATGATATTTTGGTAAACCCGAGAAATTCAGTACTAATGATGATA 618
QY 554 CTGTGATGAGAAATTCGAAATATATGTCACAGACTCTCAACGTTTCTATGAGCTTGT 613
DB 619 CTGTGATGAGAAATTCGAAATATATGTCACAGACTCTCAACGTTTCTATGAGCTTGT 678
QY 614 CTTTCTGATGCTCCGAAAGCAAGATGAGACATCTTGTGCTGCACTGAGTCAA 673
DB 679 CTTTCTGATGCTCCGAAAGCAAGATGAGACATCTTGTGCTGCACTGAGTCAA 738
QY 674 T---GAACTTCCCTCCCTACCTATATATATGAAACCAAGAGTGAAGAGAA 725
DB 739 TGGAGATGCTGCTCTCCCTACCTTCAATATATGATGCAACCAAGATGAAAGA 793

RESULT 13

AAZ27929
ID AAZ27929 standard; DNA; 2830 BP.

XX AAZ27929;

XX 20-DEC-1999 (first entry)

XX Feline B7-2 protein encoding DNA.

XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Fells catus.

XX WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX P-PSDB; AAY41079.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
PS Claim 1; Page 116-119; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The nucleic acid molecules
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match 69.3%; Score 582.2; DB 20; Length 2830;
Best Local Similarity 89.4%; Pred. No. 1.2e-161;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 14 GCACATGGAACGTAATACATTTCTTTGTATGACCTCTGCTATAGTGCCTGCT 73
DB 195 GCACATGGAACGTAATACATTTCTTTGTATGACCTCTGCTATAGTGCCTGCT 254

```

XX      Feline CD86 (B7-2) cDNA.
DE      CD86; B7-2; feline; cat; recombinant virus; vaccine;
KW      immunomodulator; tumour; cancer; therapy; ss.
XX      Fells domesticus.
OS
XX      Key      Location/Qualifiers
FH      CDS      63..1052
FT
FT      CDS      /*tag= a
XX
XX      WO9957295-A1.
XX      11-NOV-1999.
XX
XX      30-APR-1999; 99WO-US09504.
XX
XX      01-MAY-1998; 98US-0071711.
XX
XX      (SCHE ) SCHERING-PLOUGH LTD.
XX      (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX
XX      Winslow BJ, Cochran MD;
XX
XX      WPI; 2000-062155/05.
XX      P-PSDB; AAY32285.
XX
XX      Novel recombinant virus useful as immunomodulators, particularly in
XX      vaccines -
XX      Disclosure; Fig 3A; 230pp; English.
XX
XX      This is the nucleotide sequence of cDNA coding for feline CD86
XX      (B7-2). The cDNA was isolated from feline peripheral blood
XX      mononuclear cell cDNA by PCR. Manipulating the expression of CD28
XX      or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
XX      regulates T cell proliferation and cytokine release. The invention
XX      relates to a recombinant virus that contains at least one foreign
XX      nucleic acid, inserted into a nonessential genomic region, that
XX      encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
XX      immunogenic fragments, and is expressed when the recombinant virus
XX      is introduced into a suitable host. The invention also provides:
XX      a recombinant virus further comprising a foreign nucleic acid
XX      encoding an immunogen derived from a feline pathogen; recombinant
XX      viruses capable of enhancing an immune response to protect against
XX      disease; recombinant viruses expressing antisense sequences,
XX      capable of suppressing an immune response in a feline, e.g. for
XX      treatment of autoimmune disease or transplant rejection; and
XX      recombinant viruses expressing DNA encoding CD80 and/or CD86 used
XX      to reduce or eliminate a tumour in cats.
XX
XX      Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
XX
XX      Query Match      69.3%; Score 582.2; DB 21; Length 1080;
XX      Best Local Similarity 89.4%; Pred. No. 7.5e-162;
XX      Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
XX
XX      QY      14 GCACATGGAAGCTGAATACATCTCTTGTGATGACCTCTCTCTATGCTGCTCTT 73
XX      ++++++
XX      DB      79 GCACATGGAAGCTGAATACATCTCTTGTGATGACCTCTCTCTATGCTGCTCTT 138
XX      ++++++
XX      QY      74 GCATGAGAGTCAAGCATTTTCAACAGACTGGAGAACCTCCATGGCATTTTCAATT 133
XX      ++++++
XX      DB      139 CCATGAGAGTCAAGCATTTTCAACAGACTGGAGAACCTCCATGGCATTTTCAACT 198
XX      ++++++
XX      QY      134 CTCAAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 193
XX      ++++++
XX      DB      199 CTCAAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 258
XX      ++++++
XX      QY      194 TGTAGAGCTATACAGAGGCAAGAACCTCAAAATGTTCAATGCAAGATTAAGGCC 253
XX      ++++++
XX      DB      259 TGTATGAGATATTACAGAGCAAGAACCTCAAAATGTTCAATGCAATATTAAGGCC 318

```

```

QY      254 GCACAGCTTTGACAAAGACATTTGACCTGAGACTTCATTAATTCAGATCAAGGACA 313
XX      ++++++
DB      319 GTACAGAGCTTTGACAAAGACATTTGACCTGAGACTTCATTAATTCAGATCAAGGACA 378
XX      ++++++
QY      314 AGGCTTTATCATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 373
XX      ++++++
DB      379 AGGCTTTATCATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 438
XX      ++++++
QY      374 AGATGAATTTGACCTATGACCTGCTTGTCTGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 433
XX      ++++++
DB      439 AATGAGTTTCTGACCTATGACCTGCTTGTCTGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 498
XX      ++++++
QY      434 CTATAGAGCAAGAAATTTGTCATGATCAATTAATTTGACCTGCTATCATCATCAAGTTTACC 493
XX      ++++++
DB      499 CTATAGAGCAAGAAATTTGTCATGATCAATTAATTTGACCTGCTATCATCATCAAGTTTACC 558
XX      ++++++
QY      494 CAGAACCCAGAGAGATGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 553
XX      ++++++
DB      559 CAGAACCTAAGAGAGATGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 618
XX      ++++++
QY      554 CTGTGATGAAGAAATTTCAATTAATGTCAGAACCTCAACGTTTCTATGAGCTTGT 613
XX      ++++++
DB      619 CTGTGATGAAGAAATTTCAATTAATGTCAGAACCTCAACGTTTCTATGAGCTTGT 678
XX      ++++++
QY      614 CTTTCTCAGTCCCTGGAAGACAGATGAGCATCTTCTGTCTGCAACTTGAAGTCAA 673
XX      ++++++
DB      679 CTTTTCAGTCCCTGGAAGACAGATGAGCATCTTCTGTCTGCAACTTGAAGTCAA 738
XX      ++++++
QY      674 T---GAAGCTTCCCTCCCTACTTATATATAGAAACCAACAAAGTGAAGAAA 725
XX      ++++++
DB      739 TGGAGATGCTGCTCTCCCTACCTTTCAATTAATTAATGACAAACCTAAGGATTAAGA 793
XX      ++++++
XX
XX      RESULT 12
XX      AA234785
XX      ID      AA234785 standard; cDNA; 1080 BP.
XX
XX      AA234785;
XX
XX      15-FEB-2000 (first entry)
XX
XX      Cat CD86 (B7-2) cDNA.
XX
XX      CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
XX      FIV; feline leukaemia virus; feline infectious peritonitis virus;
XX      feline parvovirus; feline coronavirus; feline reovirus-3;
XX      feline rotavirus; feline coronavirus; feline syncytial virus;
XX      feline sarcoma virus; feline herpesvirus; feline Borna disease;
XX      rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
XX      parasite; autoimmune disease; transplant rejection; therapy; ss.
XX
XX      Fells domesticus.
XX
XX      Key      Location/Qualifiers
XX      FH      CDS      63..1052
XX      FT
XX      FT      CDS      /*tag= a
XX
XX      WO9957271-A2.
XX      11-NOV-1999.
XX
XX      30-APR-1999; 99WO-US09502.
XX
XX      01-MAY-1998; 98US-0071699.
XX
XX      (TEXA ) TEXAS A & M SYSTEM.
XX      COLLISON EM, HASH SM, CHOI I;
XX      WPI; 2000-052972/04.
XX      P-PSDB; AAY32278.
XX

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OY	194	TGTCAGGCGCTATACAGAGGCGCAAGGACACCCCTCAAAATGTTATCGCAAGTATAAGGCC	253
Db	197	TGTAATGAAATATTCAGAGGCGCAAGGACACCCCTCAAAATGTTATCTCAAAATPAAAGGCC	256
OY	254	GCACAAAGCTTTGCAAAAGACATTTGGAGCCCTGAGACTCATTAATATTGAGATCAAGACA	313
Db	257	GTACAAAGCTTTGCAAAAGACAACTGGAGCCCTGAGACTCCACAAATGTTTGCAGTCAAGSACA	316
OY	314	AGGGCTTGATCAATGTTTCGTTCTATCATPAAAGGCCCAAGGAGCTCGTTCCCATGCAC	373
Db	317	AGGGCACATATCACTGTTTCATTCATTATAAAGGGGCCCAAGAGCACTAGTCCCATGCAC	376
OY	374	AGATGATTTCTGACCTATACAGTGCCTTGCGTAACCTTCAGCTCAACCTCAATTAATGTAACCT	433
Db	377	AAATGATTTCTGACCTATACAGTGCCTTGCTTAACCTTCAGTCAACCTCAATTAACGTAACCT	436
OY	434	CTATATGAACAGAAAATTCGCGCATATTAATTTGACCTGCTCATCTACATCAAGGTAC	493
Db	437	CTATATGAACAGAAAATTCGGCATCATTAATTTGACCTGCTCATCTATACAGGTAC	496
OY	494	CAGAACCCAAAGAGATGATTTTTGGTAAAAAACGAGAAATTCAGATCAATGATGATA	553
Db	497	CAGAACCTTAAGAGATGATTTATTTACCTTAACACTGAGAAATTCACACTAGATGATGATA	556
OY	554	CTGTCATGAAGAAATCTCAAAATTAATGTACAGAACTGTACAAAGTTTCTATCAGACTGT	613
Db	557	CTGTCATGAAGAAATCTCAAAATTAATGTACAGAACTGTACAAAGTTTCTATCAGACTGC	616
OY	614	CTTCTCATGTCCTCGAAGCAGCAATGTGAGCATCTTCTGTGCTGCACACTTGATGCA	673
Db	617	CTTTTTCAGTCCCTCGAAGCAGCACAAATGTGAGCGCTTTTGTGCCCTCGAAACTGAGACAC	676
OY	674	T---GAAGCTTCCCTCCCTACCTTTAATATATGAAAAACAACAAGTGGAGAGAAA	725
Db	677	TGGAGATGCTGCTCTCCCTACCTTTCAATATATGATGACACAACTGAAGGATTAAGA	731
RESULT 10			
ID	AA227932/C		
XX	AA227932 standard; DNA; 996 BP.		
AC	AA227932;		
XX			
DT	20-DEC-1999 (first entry)		
XX			
DE	Complementary strand of feline B7-2 coding sequence.		
XX			
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;		
KW	allergic reaction; infectious disease; tumor development; feline;		
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.		
XX			
OS	Felis catus.		
XX			
PN	W09947558-A2.		
XX			
PD	23-SEP-1999.		
XX			
PF	19-MAR-1999; 99WO-US06187.		
XX			
PR	19-MAR-1998; 98US-0078765.		
PR	17-APR-1998; 98US-0062597.		
XX			
PA	(HESK-) HESKA CORP.		
XX			
PI	Sim G, Yang S, Sellins KS;		
XX	WPI; 1999-571822/48.		
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for		
PS	treating, e.g. autoimmune and atopic diseases -		
PS	Claim 1; Page 124-125; 148pp; English.		

Query Match	Best Local Similarity	Matches	Score	DB	Length
69.3%	89.4%	639	582.2	20	996
Conservative	Pred. No. 7.2e-162	0	Mismatches 73	Indels 3	Gaps 1
Sequence	996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;				
14	GCACATGACGATGATTAACATTTCTTTGTGATGACCCCTCTGCTATGTGCTGCTT	73			
980	GCACATGAGGACTGAGTGCACCTCTCTTTGTATGAGCCCTCTGCTCTGCTGTTCTT	921			
74	CCATGAAGCGTCAGCATTTTCAACAACAGCGAGAACTGCAAGCCATTGTACAAAT	133			
920	CCATGAAGGTCAGCATTTTCAACAACAGCTGAGAACTGCAAGCCATTGTACAACT	861			
134	CTCAAAACCTAAGCCTGGATGTGATGGTGTGTTTGGCAGGACCAAGATGCTGTTCC	193			
860	CTCAAAACCTAAGCCTGGATGTGATGGTGTGTTTGGCAGGACCAAGATGCTGTTCC	801			
194	TGTACGAGCTATACAGAGCAAGACCCCTCAAAATTTCTATGCGCAAGTAAAGGCC	253			
800	TGTATGAGATATTCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	741			
254	GCACAAAGCTTTGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	313			
740	GTACAAAGCTTTGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	681			
314	AGGCGTTGATCAATGTTCCTTCATCATTAAGAGGCCCAAGAGCTGCTCCATGACCC	373			
680	AGGCGCATATCACTGCTTCATTCATTAAGAGGCCCAAGAGCTGCTCCATGACCC	621			
374	AGATGAACTTCTGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	433			
620	AAATGAGTTCTGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	561			
434	CTAATGAAAGCAAGAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	493			
560	CTAATGAAAGCAAGAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	501			
494	CAGAACCCAGGAGATGTTTTTGGTAAAGAACCGAAGATCACTACTAGTATGATA	553			
500	CAGAACCTAAGGAGATGTTTTTGGTAAAGAACCGAAGATCACTACTAGTATGATA	441			
554	CTGTCAATGAAAGAAATTTCAAAATTAATGTCACAGAACTGTACAAAGCTTCTACAGCTGT	613			
440	CTGTCAATGAAAGAAATTTCAAAATTAATGTCACAGAACTGTACAAAGCTTCTACAGCTGT	381			
614	CCTTCTCACTCCTGAGAGCAATGTAGACATCTTGTGTCTCTGCAACTGTGATCA	673			
380	CTTTTCACTCCTGAGAGCAACAAATGTAGAGCTCTTTGTGTCTCTGCAACTGTGATCA	321			
674	T---GAAGTCTCCCTACCTATTAATATATGAAACCAAGAGGAGAGAAA	725			
320	TGAGATGCTGCTCTCTACCTTTCAATATATGATGACACAACTAAGATTAAGA	266			


```
QY 361 GTTCCATGACACAGATGAAATTCGACCTATCATGCTGTGCTACTTCACTCAACCTGAA 420
    |||||||
Db 627 GTTCCATGACACAGATGAAATTCGACCTATCATGCTGTGCTACTTCACTCAACCTGAA 568
QY 421 ATATAGTAACTTCTTAATGAAACAAAATTCGTGGCATCAATAATTTGACCTGCTCATCC 480
    |||||||
Db 567 ATATAGTAACTTCTTAATGAAACAAAATTCGTGGCATCAATAATTTGACCTGCTCATCC 508
QY 481 ATACAAAGTTACCCAGAACCCAGAGAGATGATTTTGGTAAAAAACCAGATTCAGT 540
    |||||||
Db 507 ATACAAAGTTACCCAGAACCCAGAGAGATGATTTTGGTAAAAAACCAGATTCAGT 448
QY 541 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 600
    |||||||
Db 447 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 388
QY 601 TCTATGAGCTTGTCTTCTGATGCTGCAAGCAAGCAATGAGCAATCTTCTGTGCTG 660
    |||||||
Db 387 TCTATGAGCTTGTCTTCTGATGCTGCAAGCAAGCAATGAGCAATCTTCTGTGCTG 328
QY 661 CAACCTTGAGTCAATGAGCTTCTCTCCCTACCTTATATATAGAACCAACA 712
    |||||||
Db 327 CAACCTTGAGTCAATGAGCTTCTCTCCCTACCTTATATATAGATGACACATA 276

RESULT 7
AAZ27913
ID AAZ27913 standard: DNA; 1897 BP.
XX
AC AAZ27913:
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2 protein encoding DNA.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
    allergic reaction; infectious disease; tumor development; canine;
    graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
PI
XX
DR WPI: 1999-571822/48.
XX
DR P-PSDB; AAY41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
    treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 97-99; 148pp: English.
XX
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
    encoding nucleic acid molecules from dogs and cats. The proteins can be
    expressed by standard recombinant methodology. The nucleic acid molecules
    and the encoded proteins can be used for preventing or treating diseases,
    e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
    development, graft rejection, inflammation, arthritis and atopic diseases
    such as atopic dermatitis. They can be used in mammals such humans, dogs,
    cats, cattle, sheep or pets. The products can also be used for detection,
    diagnosis and drug screening.
XX
XX Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;
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Query Match 83.8%; Score 704; DB 20; Length 1897;
Best Local Similarity 99.3%; Pred. No. 9,4e-198;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGATATCGAGATGACACTATGGAAGTGAATTAATCTCTTTGTGATGACCTCTGCTC 60
    |||||||
Db 6 ATGATATCGAGATGACACTATGGAAGTGAATTAATCTCTTTGTGATGACCTCTGCTC 65
QY 61 TATGTCGCTGCTTCCATGAGAGTCAAGCATATTTCAACAGACTGAGAGAGCCATGC 120
    |||||||
Db 66 TATGTCGCTGCTTCCATGAGAGTCAAGCATATTTCAACAGACTGAGAGAGCCATGC 125
QY 121 CATTTTACAATTTCTGAAACATAAGCCCTGATGATGTTGTATGTTTGGCAGAGCAG 180
    |||||||
Db 126 CATTTTACAATTTCTGAAACATAAGCCCTGATGATGTTGTATGTTTGGCAGAGCAG 185
QY 181 GATTAAGCTGTTCTGTATGAGCATATACAGAGSCAAGAACCCCTCAAAATGTCATCGC 240
    |||||||
Db 186 GATTAAGCTGTTCTGTATGAGCATATACAGAGSCAAGAACCCCTCAAAATGTCATCGC 245
QY 241 AAGTATTAAGGGCCGCAAGACTTTTGACAAAGCAATTTGACCTGAGACTCATATATT 300
    |||||||
Db 246 AAGTATTAAGGGCCGCAAGACTTTTGACAAAGCAATTTGACCTGAGACTCATATATT 305
QY 301 CAGATCAAGGACCAAGGGCTTTGATCAATGTTTCGTTATCAATAAAGGCCCAAGAGACTC 360
    |||||||
Db 306 CAGATCAAGGACCAAGGGCTTTGATCAATGTTTCGTTATCAATAAAGGCCCAAGAGACTC 365
QY 361 GTTCCATGACACAGATGAAATTCGACCTATCATGCTGTGCTACTTCAACCTGAA 420
    |||||||
Db 366 GTTCCATGACACAGATGAAATTCGACCTATCATGCTGTGCTACTTCAACCTGAA 425
QY 421 ATATAGTAACTTCTTAATGAAACAAAATTCGACCATTAATTTGACCTGCTCATCC 480
    |||||||
Db 426 ATATAGTAACTTCTTAATGAAACAAAATTCGACCATTAATTTGACCTGCTCATCC 485
QY 481 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGAAATTCAGT 540
    |||||||
Db 486 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGAAATTCAGT 545
QY 541 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 600
    |||||||
Db 546 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 605
QY 601 TCTATGAGCTTGTCTTCTGATGCTGCAAGCAAGCAATGAGCAATCTTCTGTGCTG 660
    |||||||
Db 606 TCTATGAGCTTGTCTTCTGATGCTGCAAGCAAGCAATGAGCAATCTTCTGTGCTG 665
QY 661 CAACCTTGAGTCAATGAGCTTCTCTCCCTACCTTATATATAGAACCAACA 712
    |||||||
Db 666 CAACCTTGAGTCAATGAGCTTCTCTCCCTACCTTATATATAGATGACACATA 717

RESULT 8
AAZ27914/c
ID AAZ27914 standard: DNA; 1897 BP.
XX
AC AAZ27914:
XX
DT 20-DEC-1999 (first entry)
XX
XX
XX Canine B7-2 gene complementary DNA sequence.
XX
DE
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
    allergic reaction; infectious disease; tumor development; canine;
    graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
```

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
PS Claim 1: Page 102-103; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 83.8%; Score 704; DB 20; Length 987;
Best Local Similarity 99.3%; Pred. No. 6, 9e-198;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACATGTAAGTAATGATTAATCTCTTTGTGATGACCTCTGCTC 60
DB 1 ATGTATCTCAGATGACATGTAAGTAATGATTAATCTCTTTGTGATGACCTCTGCTC 60
QY 61 TATGGTGTCTTCCATGAGATCAAGCATATTTCAAGACTGAGACCTGCATGC 120
DB 61 TATGGTGTCTTCCATGAGATCAAGCATATTTCAAGACTGAGACCTGCATGC 120
QY 121 CATTTTACAATTTCCAAAACATAGAGCTGGATGAGTGTGTGTTGGCAGACGAG 180
DB 121 CATTTTACAATTTCCAAAACATAGAGCTGGATGAGTGTGTGTTGGCAGACGAG 180
QY 181 GATAAGCTGTCTGTGTACAGCTATACAGAGCCAAAGAACCTCAAAATGTTATCGC 240
DB 181 GATAAGCTGTCTGTGTACAGCTATACAGAGCCAAAGAACCTCAAAATGTTATCGC 240
QY 241 AAGTATTAAGGGCCGACAAAGCTTTGACAAAGACATTTGGACCTGAGACTCCATAATATT 300
DB 241 AAGTATTAAGGGCCGACAAAGCTTTGACAAAGACATTTGGACCTGAGACTCCATAATATT 300
QY 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTGTTCATCATTAAGAGGCCCAAGGACTC 360
DB 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTGTTCATCATTAAGAGGCCCAAGGACTC 360
QY 361 GTTCCATGACGACGACATTAATTTGACCTATGAGTGTCTGCTCAATTCAGTCAACCTGAA 420
DB 361 GTTCCATGACGACGACATTAATTTGACCTATGAGTGTCTGCTCAATTCAGTCAACCTGAA 420
QY 421 AATAATGTAATCTCTAATAGAACAGAAAATTTGGCATCATTAATTTGACCTGCTCATCC 480
DB 421 AATAATGTAATCTCTAATAGAACAGAAAATTTGGCATCATTAATTTGACCTGCTCATCC 480
QY 481 ATACAGAGTTACCCGAGACCCAGAGAGATGATTTTTTGGTAAACCCGAGAAATTCACAT 540
DB 481 ATACAGAGTTACCCGAGACCCAGAGAGATGATTTTTTGGTAAACCCGAGAAATTCACAT 540
QY 541 ACTAAGTATGATCTGTATGACAGAAATTCGCAAAATATATGTCACAGAACTTACAACTT 600
DB 541 ACTAAGTATGATCTGTATGACAGAAATTCGCAAAATATATGTCACAGAACTTACAACTT 600
QY 601 TGTATCAGCTTGTCTTCTGAGTCCGTAAGCAAGCAAGTGTGAGCTGCTGCTGCTG 660
DB 601 TGTATCAGCTTGTCTTCTGAGTCCGTAAGCAAGCAAGTGTGAGCTGCTGCTGCTGCTG 660
QY 661 CAACTTGAGTCAATGAAAGCTTCCCTCTACCTTATTAATATAGAAACCAACA 712
DB 661 CAACTTGAGTCAATGAAAGCTTCCCTCTACCTTATTAATATAGATGCACATA 712

RESULT 6
AA227916/c
ID AA227916 standard; DNA; 987 BP.

XX
AC AA227916;
XX
DT 20-DEC-1999 (first entry)
XX
XX
DE Complementary strand of canine B7-2 coding sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.
PN WO947558-A2.

XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06187.

PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Sellins KS;

DR WPI; 1999-571822/48.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases

XX Claim 1: Page 103-104; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SQ Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Query Match 83.8%; Score 704; DB 20; Length 987;
Best Local Similarity 99.3%; Pred. No. 6, 9e-198;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACATGTAAGTAATGATTAATCTCTTTGTGATGACCTCTGCTC 60
DB 987 ATGTATCTCAGATGACATGTAAGTAATGATTAATCTCTTTGTGATGACCTCTGCTC 928
QY 61 TATGGTGTCTTCCATGAGATCAAGCATATTTTCAACCAAGACTGAGAACTGCCATGC 120
DB 927 TATGGTGTCTTCCATGAGATCAAGCATATTTTCAACCAAGACTGAGAACTGCCATGC 868
QY 121 CATTTTACAATTTCCAAAACATAGAGCTGGATGAGTGTGTGTTGGCAGACGAG 180
DB 867 CATTTTACAATTTCCAAAACATAGAGCTGGATGAGTGTGTGTTGGCAGACGAG 808
QY 181 GATAAGCTGTCTGTGTACAGCTATACAGAGCCAAAGAACCTCAAAATGTTATCGC 240
DB 807 GATAAGCTGTCTGTGTACAGCTATACAGAGCCAAAGAACCTCAAAATGTTATCGC 748
QY 241 AAGTATTAAGGGCCGACAAAGCTTTGACAAAGCAATTTGACCCCTGAGACTCCATAATATT 300
DB 747 AAGTATTAAGGGCCGACAAAGCTTTGACAAAGCAATTTGACCCCTGAGACTCCATAATATT 688
QY 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTCTTATCATATAAAGGCCCAAGGACTC 360
DB 687 CAGATCAAGGACAAAGGCTTGTATCAATGTTTCTTATCATATAAAGGCCCAAGGACTC 628

OY 781 GAAGCCAGTGTGTTAACTTTGCAAGACAGCTTCAGCGACAACACTACTACAGATT 840
|||||
Db 787 GAAGCCAGTGTGTTAACTTTGCAAGACAGCTTCAGCGACAACACTACTACAGATT 846

RESULT 4
AAZ27922/c
ID AAZ27922 standard; DNA: 1795 BP.

XX AAZ27922;

XX 20-DEC-1999 (first entry)

DE Canine B7-2S gene complementary DNA sequence.

XX B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

XX WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPI: 1999-571822/48.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -

PS Claim 1: Page 112-114; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SO Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;

Query Match 100.0%; Score 840; DB 20; Length 1795;

Best Local Similarity 100.0%; Pred. No. 5,6e-238;

Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTATCTCAGATGACACTGTGAGTGAATTAACATCTCTTGTGAGCCCTGCTGTC 60
|||||

Db 1789 ATGTATCTCAGATGACACTGTGAGTGAATTAACATCTCTTGTGAGCCCTGCTGTC 1730

OY 61 TATGTGCTGCTTCCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
|||||

Db 1729 TATGTGCTGCTTCCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 1670

OY 121 CATTTTACAATTCGCAAAACATAAGCCTGGATGATGTTGGTGTGTTGGCAGGACAG 180
|||||

Db 1669 CATTTTACAATTCGCAAAACATAAGCCTGGATGATGTTGGTGTGTTGGCAGGACAG 1610

OY 181 GATTAAGCTGTTCTGTAGAGCTATTAACAGAGCAAGAAACCTCAAAATGTTCAATGC 240
|||||

Db 1609 GATTAAGCTGTTCTGTAGAGCTATTAACAGAGCAAGAAACCTCAAAATGTTCAATGC 1550

OY 241 AAGTATPAGGGCCGACAGCTTTTGACAAAGACATTTGGACCTGAGACTCCATATATP 300
|||||

Db 1349 AAGTATPAGGGCCGACAGCTTTTGACAAAGACATTTGGACCTGAGACTCCATATATP 1490

OY 301 CAGATCAAGGACAGGGGCTTGTATCAATGTTTGGTCACTATAAGGCCCAAGAGACTC 360
|||||

Db 1489 CAGATCAAGGACAGGGGCTTGTATCAATGTTTGGTCACTATAAGGCCCAAGAGACTC 1430

OY 361 GTTCCCATGACACAGATGAAATTCGACCTATGACCTGCTTGGCTTAAGTCAACCTGAA 420
|||||

Db 1429 GTTCCCATGACACAGATGAAATTCGACCTATGACCTGCTTGGCTTAAGTCAACCTGAA 1370

OY 421 ATATGCTAACTTCTAAT76GAACAGAAAATTTGGCATCATAAATTTGACTGCTCATCC 480
|||||

Db 1369 ATATGCTAACTTCTAAT76GAACAGAAAATTTGGCATCATAAATTTGACTGCTCATCC 1310

OY 481 ATCAAGGTTACCCAGAACCCCAAGGAGATGATTTTGGTAAACCGAATTCAGT 540
|||||

Db 1309 ATCAAGGTTACCCAGAACCCCAAGGAGATGATTTTGGTAAACCGAATTCAGT 1250

OY 541 ACTAAGTATGATCTGTCTATGAAGAAATCTCAAAATATGTCACAGAACTTCACAGTT 600
|||||

Db 1249 ACTAAGTATGATCTGTCTATGAAGAAATCTCAAAATATGTCACAGAACTTCACAGTT 1190

OY 601 TCTATCAGCTTGTCTTCTCATAGTCCCTGAGCAAGCAATGTGACATCTGTGCTCTG 660
|||||

Db 1189 TCTATCAGCTTGTCTTCTCATAGTCCCTGAGCAAGCAATGTGACATCTGTGCTCTG 1130

OY 661 CAACCTTAGTCATGAAAGCTTCCCTCCCTACTTAAATATGAAACCAACAAAGTGAAG 720
|||||

Db 1129 CAACCTTAGTCATGAAAGCTTCCCTCCCTACTTAAATATGAAACCAACAAAGTGAAG 1070

OY 721 AGAAAGAAAGTGAGCAGACCAAGAAAGTACCGTACCATGGAAGGAAATCTGAT 780
|||||

Db 1069 AGAAAGAAAGTGAGCAGACCAAGAAAGTACCGTACCATGGAAGGAAATCTGAT 1010

OY 781 GAAGCCAGTGTGTTAACTTTGCAAGACAGCTTCAGCGACAACACTACTACAGATT 840
|||||

Db 1009 GAAGCCAGTGTGTTAACTTTGCAAGACAGCTTCAGCGACAACACTACTACAGATT 950

RESULT 5

AAZ27915
ID AAZ27915 standard; DNA: 987 BP.

XX AAZ27915;

XX 20-DEC-1999 (first entry)

DE Canine B7-2 protein coding sequence.

KW B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; canine;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

XX WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPI: 1999-571822/48.

XX P-PSDB: AAY41076.

```
OY 241 AAGTAAAGGGCCGACAAAGCTTTGACAAAGACAAATTGACCCCTGAGACTGCATATATTT 300
    |||
DB 600 AAGTAAAGGGCCGACAAAGCTTTGACAAAGACAAATTGACCCCTGAGACTGCATATATTT 541
OY 301 CAGATCAAGGACAAAGGCTTTGATCAATGTTTGGCTATCATATTAAGGGCCCAAGAGACTC 360
    |||
DB 540 CAGATCAAGGACAAAGGCTTTGATCAATGTTTGGCTATCATTAAGGGCCCAAGAGACTC 481
OY 361 GTTCCATGACACAGATGAATTTGACCTATTCAGCTGCTTCTTAATTCAGTCAACCTGAA 420
    |||
DB 480 GTTCCATGACACAGATGAATTTGACCTATTCAGCTGCTTCTTAATTCAGTCAACCTGAA 421
OY 421 ATAAATGTAACCTTCTAATAGAAAGAAATTTGGGCTATCAATTAATTTGACCTGCTATCC 480
    |||
DB 420 ATAAATGTAACCTTCTAATAGAAAGAAATTTGGGCTATCAATTAATTTGACCTGCTATCC 361
OY 481 ATACAAAGGTTACCCGAAACCCAGAGAGATGATTTTGTGTAAGAAACGAGAAATTCAGT 540
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DB 360 ATACAAAGGTTACCCGAAACCCAGAGAGATGATTTTGTGTAAGAAACGAGAAATTCAGT 301
OY 541 ACTAAGTATGATCTGTCATAGAAATTCCTCAAAATATGTCACAGACTGACAACTG 600
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DB 300 ACTAAGTATGATCTGTCATAGAAATTCCTCAAAATATGTCACAGACTGACAACTG 241
OY 601 TCTATCAGCTGTCTCTCTCTCAGTCCCTGAAGCAAGCAATGTGACATCTTCTGTCTG 660
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DB 240 TCTATCAGCTGTCTCTCTCTCAGTCCCTGAAGCAAGCAATGTGACATCTTCTGTCTG 181
OY 661 CAACCTGAGTCAATGAACTTCCTCCCTACCTTAAATTAAGAACCAACAAAGTGAG 720
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DB 180 CAACCTGAGTCAATGAACTTCCTCCCTACCTTAAATTAAGAACCAACAAAGTGAG 121
OY 721 AGAAAAAGAAAGTAGACAGACCAAGAAAGAGTAGAGTACCATGAAGCGAAAGATCTGAT 780
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DB 120 AGAAAAAGAAAGTAGACAGACCAAGAAAGAGTAGAGTACCATGAAGCGAAAGATCTGAT 61
OY 781 GAAGCCGAGTGTGAATTCGAATTCGACAGCAAGCTTCAGGCGACAAAGTACTACAGTTT 840
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DB 60 GAAGCCGAGTGTGAATTCGAATTCGACAGCAAGCTTCAGGCGACAAAGTACTACAGTTT 1

RESULT 3
AAZ27921
ID AAZ27921 standard; DNA; 1795 BP.
XX
AC AAZ27921;
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein encoding DNA.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PE 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
DR P-PSDB; AAY41078.
XX
```

```
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 109-111; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;
XX
Query Match 100.0%; Score 840; DB 20; Length 1795;
Best Local Similarity 100.0%; Pred. No. 5,6e-238;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATATATCTCAGTATGCACATATGSACTGATATACATTTCTCTTTGTGATGACCTCTGCTC 60
    |||
DB 7 ATGATATCTCAGATGCACTATGSACTGATATACATTTCTCTTTGTGATGACCTCTGCTC 66
OY 61 TATGTCGTCTCTCCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
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DB 67 TATGTCGTCTCTCCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 126
OY 121 CATTTTCAAAATTTCAAAACATTAAGCTGATGAGTTGTAGTGTGTTGGCAGACAG 180
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DB 127 CATTTTCAAAATTTCAAAACATTAAGCTGATGAGTTGTAGTGTGTTGGCAGACAG 186
OY 181 GATPAGCTGTTCTGTAGAGCTATATGAGAGCAAGAAACCTTCAAATTTGTCATCC 240
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DB 187 GATPAGCTGTTCTGTAGAGCTATATGAGAGCAAGAAACCTTCAAATTTGTCATCC 246
OY 241 AACTATPAGGGCCGACAGAGCTTTGACAAAGACAAATTTGACCTGACATCTCAATATT 300
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DB 247 AACTATPAGGGCCGACAGAGCTTTGACAAAGACAAATTTGACCTGACATCTCAATATT 306
OY 301 CAGATCAAGGACAAAGGCTTTGATCAATGTTTGGTATCATTAAGGGCCCAAGAGACTC 360
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DB 307 CAGATCAAGGACAAAGGCTTTGATCAATGTTTGGTATCATTAAGGGCCCAAGAGACTC 366
OY 361 GTTCCATGACACAGATGAATTTGACCTATTCAGCTGCTTCTTAATTCAGTCAACCTGAA 420
    |||
DB 367 GTTCCATGACACAGATGAATTTGACCTATTCAGCTGCTTCTTAATTCAGTCAACCTGAA 426
OY 421 ATAAATGTAACCTTCTAATAGAAAGAAATTTGGGCTATCAATTAATTTGACCTGCTATCC 480
    |||
DB 427 ATAAATGTAACCTTCTAATAGAAAGAAATTTGGGCTATCAATTAATTTGACCTGCTATCC 486
OY 481 ATACAAAGGTTACCCGAAACCCAGAGAGATGATTTTGTGTAAGAAACGAGAAATTCAGT 540
    |||
DB 487 ATACAAAGGTTACCCGAAACCCAGAGAGATGATTTTGTGTAAGAAACGAGAAATTCAGT 546
OY 541 ACTAAGTATGATCTGTCATAGAAATTCCTCAAAATATGTCACAGACTGACAACTG 600
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DB 547 ACTAAGTATGATCTGTCATAGAAATTCCTCAAAATATGTCACAGACTGACAACTG 606
OY 601 TCTATCAGCTGTCTCTCTCTCAGTCCCTGAAGCAAGCAATGTGACATCTTCTGTCTG 660
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DB 607 TCTATCAGCTGTCTCTCTCTCAGTCCCTGAAGCAAGCAATGTGACATCTTCTGTCTG 666
OY 661 CAACCTGAGTCAATGAACTTCCTCCCTACCTTAAATTAAGAACCAACAAAGTGAG 720
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DB 667 CAACCTGAGTCAATGAACTTCCTCCCTACCTTAAATTAAGAACCAACAAAGTGAG 726
OY 721 AGAAAAAGAAAGTAGACAGACCAAGAAAGAGTAGAGTACCATGAAGCGAAAGATCTGAT 780
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DB 727 AGAAAAAGAAAGTAGACAGACCAAGAAAGAGTAGAGTACCATGAAGCGAAAGATCTGAT 786
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PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 114; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX

Sequence 840 BP; 278 A; 181 C; 167 G; 214 T; 0 other;

Query Match 100.0%; Score 840; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;

Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCTCGATGCACTATGAACTGAATACATTCCTTGTGATGACCCCTCCGCTC 60
DB 1 ATGATCTCGATGCACTATGAACTGAATACATTCCTTGTGATGACCCCTCCGCTC 60
QY 61 TATGCTGCTCTTCATGAAAGTCAAGCATATTTCCACAGACTGAGAACCTGCATGC 120
DB 61 TATGCTGCTCTTCATGAAAGTCAAGCATATTTCCACAGACTGAGAACCTGCATGC 120
QY 121 CATTTTACAATTTCTCAAAACATAGCTGGATGAGTGTGTTGGCAGACCGAG 180
DB 121 CATTTTACAATTTCTCAAAACATAGCTGGATGAGTGTGTTGGCAGACCGAG 180
QY 181 GATAAGCTGGTCTGTACGAGCTATACAGAGCAAGCAACCTCAAAATGTTCAATCC 240
DB 181 GATAAGCTGGTCTGTACGAGCTATACAGAGCAAGCAACCTCAAAATGTTCAATCC 240
QY 241 AAGTAAAGGCGCCACACAGCTTTGACAAAGACATTTGACCCCTGAGCTCATAATAT 300
DB 241 AAGTAAAGGCGCCACACAGCTTTGACAAAGACATTTGACCCCTGAGCTCATAATAT 300
QY 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGTCATCATTAAGAGGCCCAAGAGACATC 360
DB 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGTCATCATTAAGAGGCCCAAGAGACATC 360
QY 361 GTTCCCATGACAGATGATTTCTGACCTTCAGTCTTCTCACTCACTCACTGAA 420
DB 361 GTTCCCATGACAGATGATTTCTGACCTTCAGTCTTCTCACTCACTCACTGAA 420
QY 421 ATAAATGTAATCTTAATAGACAGAAAATTTGGCATCATTAATTTGACCTGCTATCC 480
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QY 481 ATCAAGGTTACCCAGAACCCAGAGATGATATTTTGTAAACCCGAGATTTCAAG 540
DB 481 ATCAAGGTTACCCAGAACCCAGAGATGATATTTTGTAAACCCGAGATTTCAAG 540
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QY 601 TCTATGAGCTTGTCTCTGAGTCCCTGAAGCAAGCAATGTGAGCATTTCTGTGCTG 660
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QY 661 CAACTTGAAGTCAAGAGCTTCCCTCCCTACCTTATATATAGAAACCAAGAGTGGAG 720
DB 661 CAACTTGAAGTCAAGAGCTTCCCTCCCTACCTTATATATAGAAACCAAGAGTGGAG 720
QY 721 AGAAAGAAAGTGAAGCAAGCAAGAGAGTACGATACATGAAGCAAGAAATGTCAT 780
DB 721 AGAAAGAAAGTGAAGCAAGCAAGAGAGTACGATACATGAAGCAAGAAATGTCAT 780

QY 781 GAAGCCAGTGTGTTAACTTTCCAGACAGCTTCAGGCGCAACAGTACTACAGATT 840
DB 781 GAAGCCAGTGTGTTAACTTTCCAGACAGCTTCAGGCGCAACAGTACTACAGATT 840

RESULT 2

AAZ27924/C
ID AAZ27924 standard; DNA; 840 BP.

AAZ27924;

20-DEC-1999 (first entry)

Complementary strand of canine B7-2S coding sequence.

KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

PN W09947558-A2.

PD 23-SEP-1999.

PF 19-MAR-1999; 99WO-US06187.

PR 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

PA (HESKA -) HESKA CORP.

PI Sim G, Yang S, Sellins KS;

DR WPI; 1999-571822/48.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX

PS Claim 1; Page 115; 148bp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX

Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;

Query Match 100.0%; Score 840; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;

Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCTCGATGCACTATGAACTGAATACATTCCTTGTGATGACCCCTCCGCTC 60
DB 840 ATGATCTCGATGCACTATGAACTGAATACATTCCTTGTGATGACCCCTCCGCTC 781
QY 61 TATGCTGCTCTTCATGAAAGTCAAGCATATTTCCACAGACTGAGAACCTGCATGC 120
DB 780 TATGCTGCTCTTCATGAAAGTCAAGCATATTTCCACAGACTGAGAACCTGCATGC 721
QY 121 CATTTTACAATTTCTCAAAACATAGCTGGATGAGTGTGTTGGCAGACCGAG 180
DB 720 CATTTTACAATTTCTCAAAACATAGCTGGATGAGTGTGTTGGCAGACCGAG 661
QY 181 GATAAGCTGGTCTGTACGAGCTATACAGAGCAAGAGCAACCTCAAAATGTTCAATGC 240
DB 660 GATAAGCTGGTCTGTACGAGCTATACAGAGCAAGAGCAACCTCAAAATGTTCAATGC 601

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 126.99 Seconds

(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-19

Perfect score: 840
Sequence: 1 atgcatctcagatgcactat.....acaacagctactacagcttt 840

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	840	100.0	840	AAZ27923	Canine B7-2S prote
2	840	100.0	840	AAZ27924	Complementary stra
3	840	100.0	1795	AAZ27921	Canine B7-2S prote
4	840	100.0	1795	AAZ27922	Canine B7-2S gene
5	704	83.8	987	AAZ27915	Canine B7-2 protei
6	704	83.8	987	AAZ27916	Complementary stra
7	704	83.8	1897	AAZ27913	Canine B7-2 protei
8	704	83.8	1897	AAZ27914	Canine B7-2 gene c
9	582.2	69.3	996	AAZ27931	Feline B7-2 protei

C	10	582.2	69.3	996	20	AAZ27932	Complementary stra
	11	582.2	69.3	1080	21	AAZ34838	Feline CD86 (B7-2)
	12	582.2	69.3	1080	21	AAZ34785	Cat CD86 (B7-2) cD
	13	582.2	69.3	2830	20	AAZ27929	Feline B7-2 protei
C	14	582.2	69.3	2830	20	AAZ27930	Feline B7-2 gene c
	15	485	57.7	1050	21	AAZ49661	Pig costimulatory
	16	484.6	57.7	764	18	AAZ62939	Chimeric human/por
	17	463.8	55.2	831	19	AAV03230	DNA encoding CD86
	18	463.8	55.2	1130	16	AAQ81351	Human B lymphocyte
	19	463.8	55.2	1130	18	AAZ49181	Human B lymphocyte
	20	463.8	55.2	1120	20	AAV55784	Human B7-2 antigen
	21	463.8	55.2	1120	21	AAZ84049	Human B lymphocyte
	22	458.8	54.6	1124	21	AAZ29321	Human B7-2 cDNA.
	23	458.8	54.6	1428	16	AAQ85873	B70 type B antigen
	24	458.8	54.6	2205	22	AAH72616	Human cervical can
	25	453.8	54.0	738	22	AAV80293	Human B7-2 extrace
	26	453.8	54.0	738	22	AAZ89731	Nucleotide sequenc
	27	453.8	54.0	972	20	AAV83308	B7-2 cDNA. Homo s
	28	453.8	54.0	972	24	AAZ25510	Human co-stimulat
	29	344.4	41.0	1131	20	AAV55785	Mouse B7-2 antigen
	30	344.4	41.0	1163	18	AAZ49182	Mouse B lymphocyte
	31	344.4	41.0	1163	21	AAZ84050	Murine B lymphocy
	32	342.8	40.8	1163	16	AAQ81366	Murine B lymphocy
	33	337.2	40.1	1261	16	AAZ01046	Mouse B7-2 exons m
	34	317.8	37.8	942	19	AAZ99826	Rat CD86 coding se
	35	271	32.3	359	20	AAZ27935	Feline B7-2 protei
C	36	271	32.3	359	20	AAZ27936	EST clone CR506.
	37	265.8	31.6	403	20	AAV89569	Human B lymphocyte
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	40	218	26.0	430	21	AAZ00427	Human secreted pro
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	43	169.6	20.2	509	20	AAZ27933	Feline B7-2 protei
C	44	169.6	20.2	509	20	AAZ27934	Feline B7-2 gene (
	45	86.4	10.3	210	16	AAZ01038	Human B7-2 exon 5.

ALIGNMENTS

RESULT 1	AAZ27923	standard; DNM; 840 BP.
ID	AAZ27923	
XX	AC	AAZ27923;
XX	AC	AAZ27923;
DT	20-DEC-1999	(first entry)
XX	XX	
DE	Canine B7-2S protein coding sequence.	
XX	XX	
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
KW	allergic reaction; infectious disease; tumor development; canine;	
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
XX	XX	
OS	Canis familiaris.	
XX	XX	
PN	WO9947558-A2.	
XX	XX	
PD	23-SEP-1999.	
XX	XX	
PF	19-MAR-1999;	99WO-US06187.
XX	XX	
PR	19-MAR-1998;	98US-0078765.
PR	17-APR-1998;	98US-0062597.
XX	XX	
PA	(HESK-) HESKA CORP.	
XX	XX	
PI	Sim G, Yang S, Sellins KS;	
XX	XX	
DR	WPI; 1999-571822/48.	
XX	XX	
DR	P-PSDB; AAY41078.	
XX	XX	

High quality sequence stop: 400.

FEATURES

source

Location/Qualifiers

1..570

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1634297"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was from

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and cloneids: Soares NBHSF pool 1:

309384-310919, 323208-325895 Soares NB2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 107 c 134 g 179 t

ORIGIN

Query Match 9.6%; Score 81; DB 9; Length 570;

Best Local Similarity 73.3%; Pred. No. 1.2e-09;

Matches 118; Conservative 0; Mismatches 40; Indels 3; Gaps 1;

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DB 453 CCTCGCACTTATATATATGTGACCAACATGAGAGGAGAGAGTGAACAGCA 394
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 743 AGGAAGAGTACGATGATGAAAGCGAAGATCTGATGAGCCAGTGTG--TTAACA 799
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DB 393 AGAAAGAGAGAAAAATCCATATACCTGAAAGATGATGAAACCCAGCGTGTTTAAAA 334
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QY 800 TTTCGAAGACGCTTCAGCGACACACAGTACTACACAGTTT 840
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DB 333 GTTCGAGACATCTTCATGCGACAAAGTATACATGTTT 293
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Search completed: October 20, 2002, 04:29:47

Job time : 1010.13 secs

KEYWORDS	EST
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)
AUTHORS	Marras,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person ,E., Kohn,S., Shin,T., Jackson,T., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watsn.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1010544 Seq primer: custom primer used High quality sequence stop: 285. Location/Qualifiers 1. .380 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:2317900" /clone_lib="Sugano mouse liver mlia" /sex="Female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: liver; Vector: pME18S-FL3; Site:1: Drail1 (CACCTGTG); Site 2: Drail1 (CACCTGTG); 1st strand cDNA was primed with an oligo (dtp) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a Drail1 adaptor (TGTGGCTTACTGG), digested and cloned into distinct Drail1 sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTTAACACTGG and 3' end primer CGACCTCAGCTCGACACA." BASE COUNT 99 a 87 c 102 g 90 t 2 others
ORIGIN	
Query Match	11.8%; Score 99.2; DB 9; Length 380;
Best Local Similarity	72.1%; Pred.No.3,4e-14;
Matches 142; Conservative	0; Mismatches 54; Indels 1; Gaps 1.
1	ATGTATCTCAGATGACACTGATGAATTAACATTTCTTTTGTGATGACCCCTCGCTC 60
116	ATGGAGCCCAAGATGACCATGGGCTTGGCAATCCATTATCTTTGTGACACTGTGATGC 175
61	TATGTGCTGCTTCATGAGAGTCAAGCATTTTCAACAAGACGTGAGAACTGCATGC 120
176	TCAGATGCTGTTCCGTGGAGCGCAAGCTTATTTTCAATGAGGACGTGCAATATCTGGCCTG 235
121	CATTTTACAATTTCTCAACACATTAAGCCCTGAGATGAG-TTGAGTACGTTTGGCAGAGCA 179
236	CCATTTACAAAGGCTCAAAAACATTAAGCCTGAGTGGAGCTGGTAGTATTTTGGCAGAGCA 295
180	GGATAAGCTGTCTCT 196
296	CAAAAGTTGGTTTCT 312

[illegible]

ACCESSION AA056905 Counter-receptor, human, mRNA sequence.
 VERSION AA056905.1 GI:1549545
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS Tugue, C.K., Wahls, S. and Schmitz, C.
 TITLE Expressed Sequence Tags from Pig Spleen
 JOURNAL Unpublished (1996)
 COMMENT Contact: Tugue CK
 Molecular Genetics Laboratory, Department of Animal Science
 Iowa State University
 201 Kildee Hall, Ames, IA 50011-3150, USA
 Tel: 5152944252
 Fax: 5152942401
 Email: cktugue@iastate.edu
 PCR Primers
 FORWARD: TGGGACGACTCCTG
 BACKWARD: GACCGGCGCTCAGCT
 Insert Length: 950 Std Error: 50.00
 Seq primer: TGGGACGACTCCTG.
 Location/Qualifiers
 1..512
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="SPL224"
 # PL1006b) "Pig Spleen lambda gt 11 Library (Clontech Cat
 /tissue_type="spleen"
 /dev_stage="adult"
 /note="Oligo (dnt) primed"
 BASE COUNT 125 a 106 c 114 g 163 t 4 others
 ORIGIN
 Query Match 13.8%; Score 115.8; DB 9; Length 512;
 Best Local Similarity 75.3%; Pred. No. 2.0e-18;
 Matches 171; Conservative 0; Mismatches 49; Indels 7; Gaps 2;
 QY 490 TACCCAGAACCCGAGAGATGATTTTGGTAAACCGAATTCAGTCACTAAT 549
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 512 TACCCAGAACCCGAGAGATGATTTTGGTAAATGCAAGATTCACACCTGACAT 453
 QY 550 GATCTGTGATGAGAAATCTCAAAATATGTACAGACTTACACGTTTCTATCAGC 609
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 452 GATCTGTACATGAGAAATCTCAAAATATGATCAGC--GGATTTTACATGTATCAATCAGG 394
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 610 TTGTCTTCTCAGTCCCTGGAAGCAATGTGAGCATCTTCTGTGCTGCGCAACTTGAG 669
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 393 GTGTCTCTTCCCATCCTCCCGAGACAAATGTGACATNGTCTGTGCTGCAACTTGAG 334
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 670 TCAATGAA-----GCTTCCCTCCCTTACCTTAAATATAGAAACCA 710
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 333 CCAAGCAAGACACTGCTTTCTCCCTTGTGATTAATATAGTCAAA 287
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 10
 BFL171298
 LOCUS BFL171298 314 bp mRNA linear EST 23-MAR-2001
 DEFINITION PCL2416 Myeloma (PCL) cDNA library Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION BFL171298
 VERSION BFL171298.1 GI:13437512
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 314)
 AUTHORS Claudio, J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E., Francisco-Pabalan, O., Liew, C.C. and Stewart, A.K.

TITLE The transcriptional phenotype of myeloma cells
 JOURNAL Unpublished (2000)
 COMMENT Contact: A. Keith Stewart, M.D.
 Oncology Research
 University Health Network
 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
 Tel: (416) 946-4639
 Fax: (416) 946-6546
 Email: k.stewart@utoronto.ca
 PCR Primers
 FORWARD: 5'-GCCAAGCTCGAAATTAACCTGACTTAAGG-3'
 BACKWARD: 5'-CCAGTGAATGTGATATACAGCTACATATGAGCG-3'
 Seq primer: 5'-GAAATTAACCTGACTTAAGG-3'.
 Location/Qualifiers
 1..314
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Myeloma (PCL) cDNA library"
 /sex="male"
 /tissue_type="Blood"
 /cell_type="Myeloma"
 /dev_stage="Plasma cell leukemia"
 /note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from plasma cell leukemia patient's peripheral blood containing >95% myeloma. An oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and 1a-32P[dATP] was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated and followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10⁶. Clones from the primary library were randomly selected for single pass sequencing."
 BASE COUNT 68 a 70 c 74 g 102 t
 ORIGIN
 Query Match 12.4%; Score 104.2; DB 10; Length 314;
 Best Local Similarity 77.3%; Pred. No. 1.9e-15;
 Matches 140; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 14 GCACATATGACATGATTAACATCTTCTTGTGATGACCTCTGCTATGCTGCTT 73
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 125 GCACATATGGAGCTGATTAACATCTTCTTGTGATGAGCCCTCTGCTGCTGCTT 184
 QY 74 CCATGAGAGTGCACATATTTCAACAAGACTGAGACTGCCATTCATTTTACAAATT 133
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 185 CTTGTAGGATTTAGCTTATTTATAGAGCTC---AGACCTGCCAGCCAAATTTGCAACT 241
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 134 CTCAAAACATTAAGCTGATGAGTTGTTGGCAGACCCAGATATGCTGTTTC 193
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 242 CTCAAAACCAAGCCTGATGAGTAGTAGTATTTTGGCAGACCCAGAAACATGCTTC 301
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 194 T 194
 |||||
 Db 302 T 302
 |||||
 RESULT 11
 AM260541
 LOCUS AM260541 380 bp mRNA linear EST 23-DEC-1999
 DEFINITION um83a03.y1 Sugano mouse liver m1a Mus musculus cDNA clone
 IMAGE:2317900 5' similar to gb:125606 Murine B7-2 mRNA, complete
 cds (MUSEF); mRNA sequence.
 ACCESSION AM260541
 VERSION AM260541.1 GI:6633522

Oy	598	GTCATACAGCTGCGTTCATGCATTCAAGC 631
Dd	663	ATCCACAAGGCTCTCTTTCACTTCCCAGATG 636
RESULT 6	BK089797	578 bp MRNA linear EST 19-NOV-2001
LOCUS	BM089797	
DEFINITION	503667 MARC 2Bov Bos taurus cDNA 5', mRNA sequence.	
ACCSSION	BM089797	
VERSION	BM089797.1	GI:17000425
KEYWORDS	EST.	
SOURCE	Cow.	
ORGANISM	Bos taurus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos. 1 (bases 1 to 578)	
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Faurekrug,S.C., Bennett, .G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlee,G., Holt,I., Karamecheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.	
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	
MEDLINE	21180013	
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt trimmed with phred v0.960904.e. Vector identified by cross_match with the minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAACAGCATGTGACCAT BACKWARD: GTTTCCTTGATGGAGGACG Plate: 5 row: D column: 18 Seq primer: ATTAGGTGACACTAATG. Location/Qualifiers 1..578 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC_2BOV" /tissue_type="Pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI; library made from pooled tissue from testis, thymus, semiteendonous muscle, longissimus muscle, pancreas, adrenal, and endometrium."	
FEATURES	BASE COUNT	170 a 150 c 120 g 137 t 1 others
SOURCE	ORIGIN	
Query Match	30.6%; Score 257.2; DB 10;	Length 578;
Best Local Similarity	76.9%; Pred. No. 2,7e-53;	
Matches 344;	Conservative 0;	Mismatches 83; Indels 22; Gaps 2;
Oy	1	ATGTAATCAGATGACATAAGAACTAATCTCTTTGTATGATGACCTCGTGC TC 60
Dd	124	ATGCGTTCAAATGACACATGCGAGCAAACTAATCGTAATGCGGCCCTCGTC TC 183
Oy	61	TAT-----GTCGCTGCTTCCAT-GAAGAAGCAAGCANATTTCCA 98
Dd	184	TCTGTTCCACTGCTTCCTTTTTCAAGTCTCTCTTCCTTNAAAAGTCATGCTTCTTCA 243
Oy	99	CAGACTGGAAGACTGCCATGCACTATTACAAATTCTCAAAAAACATAAGCCTGGATGATT 158
Dd	244	CGAAGCTGGAGAACCTGCATGCACTTTCCAACACCAAAACCTCACGCTGGAGCAACT 303
Oy	159	GATGATGTTTGGCAGGACCAAGATAAAGCTGTTCTGTACGAGCTATACAGAGCAAAAGA 218

Db	Accession	Source	Organism	Version	Keywords	Reference	Authors	Title	Journal	Comment
Db	304	GGTATATTTTGGCAGATCATCAATTAATTTGGTCTCTATGAGCTATTCGAAGGCCAAGA	363							
Oy	219	GAACCTCAAAATGTTTCATGCGAAGTAAAGAGGCCGACACAAGCTTTGACAAAGACAATG	278							
Db	364	GAACCCCAATTAATGTTAAATCCAAATTAATAGGCGGACAGCTTTGACAGACAGTTG	423							
Oy	279	GACCTGACAGCTCCATTAATATTCACATCAAGAGACAGAGGCTTTATCAATATGTTGGTTCA	338							
Db	424	GACCTGAGCTCCACAAAGCTTCAATATCAATCAAGACAGAGCTGATATCAATATGTTATCCA	483							
Oy	339	TCATAAAGAGGCCCAAGAGACCTGCTTCCATGACACCAATATATTCGACCTATACGTCT	398							
Db	484	TCATAGAAGGTCCCAAGAGATGTTGTTCCATCCACCAATATATGATGTTCTGACCTGATATGCT	543							
Oy	399	TGCTAACTTACGTCAACCTGAAATTAATGTAATCT	432							
Db	544	GGCTAACTTCAGTCAACCAAGAAATTAAGCTATTT	577							
RESULT 7										
LOCUS	BB635605	654 bp	mRNA	linear	EST 26-Oct-2001					
DEFINITION	BB635605	RIKEN full-length enriched, 0 day neonate thymus Mus musculus cDNA clone A430076L06 5', mRNA sequence.								
ACCESSION	BB635605									
VERSION	BB635605.1	GI:16471650								
KEYWORDS	EST.									
SOURCE	house mouse.									
ORGANISM	Mus musculus									
REFERENCE	Ekusayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 654)									
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.									
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)									
JOURNAL	Unpublished (2001)									
COMMENT	Contact: Yoshinori Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10): 1617-1630 (2000) Wagui,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Itoneda,T., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A., and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11): 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y. Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2): 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)									

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MGC Library."

BASE COUNT 227 a 166 c 156 g 204 t

ORIGIN

Query Match 48.9%; Score 410.6; DB 10; Length 753;

Best Local Similarity 82.5%; Pred. No. 2.9e-91;

Matches 519; Conservative 0; Mismatches 104; Indels 6; Gaps 4;

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QY 1 ATGATACCTAGATGCACTGATGAGTAATACATTCCTCTTGTGATGACCTCTGCTC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 107 ATGATGCCCAAGGACGACTAGGAGCTAGTAACATTCCTCTTGTGATGACCTCTGCTC 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TATGTCGTCTCTCCATGAGAGTCAAGCATATTCACAGACTGGAGACTGCCATGC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 TCTGGTGTCTCTCTCTGTAAGATTCAGCTTATTCATGATGACAGACTGCCATGC 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CATTTTACAATTCCTCAAAACATTAAGCTCGATGAGTGTGTGTGGGAGGACCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 CAATTTGCAAACTCTCAAAACCAAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GATAAGCTGGTCTGTAGACGCTATACAGAGGCAAGAG-AAOCCCTCAAAATGTTTATCG 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 GAAACTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 CAGATATAGGCGCGCAAGACTTTTACAAAGACATTTGGACCTGAGACTCCATATAT 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 CAAATATATGCGCGCGCAAGACTTTTATGATGATGATGATGATGATGATGATGATG 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 TCAGATCAAGGACAGGCGCTGTATGATGATGATGATGATGATGATGATGATGATG 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 407 TCAGATCAAGGACAGGCGCTGTATGATGATGATGATGATGATGATGATGATGATG 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 CGTTCCTGACACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 419
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 467 GATTCGATCCACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 420 AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 527 AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 480 CATACAGGTTATCCAGACCAAGAGATGATGATGATGATGATGATGATGATGATG 539
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 584 TATACAGGTTATCCAGACCAAGAGATGATGATGATGATGATGATGATGATGATG 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 540 TACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 598
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 643 TATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 599 TTTCATCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 703 TTTCATCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 2
B1824940 655 bp mRNA linear EST 04-OCT-2001
LOCUS 60303255AF1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173789 5',
DEFINITION mRNA sequence.

ACCESSION B1824940
VERSION B1824940.1 GI:15936490
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 655)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9abps-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM1432 row: 1 column: 14
High quality sequence start: 27
High quality sequence stop: 653.

FEATURES

source

1. 655

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5173789"

/clone_1b="NIH_MGC_115"

/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector:

PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH-MGC Library."

BASE COUNT 194 a 147 c 145 g 169 t

ORIGIN

Query Match 42.6%; Score 358; DB 10; Length 655;

Best Local Similarity 82.7%; Pred. No. 3e-78;

Matches 422; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

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QY 1 ATGATACCTAGATGCACTGATGAGTAATACATTCCTCTTGTGATGACCTCTGCTC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 ATGATGCCCAAGGACGACTAGGAGCTAGTAACATTCCTCTTGTGATGACCTCTGCTC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TATGTCGTCTCTCCATGAGAGTCAAGCATATTCACAGACTGGAGACTGCCATGC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 TCTGGTGTCTCTCTCTGTAAGATTCAGCTTATTCATGATGAGACTGCCATGC 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CATTTTACAATTCCTCAAAACATTAAGCTCGATGAGTGTGTGTGGGAGGACCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 CAATTTGCAAACTCTCAAAACCAAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GATTAAGCTGTCTGTAGACGCTATACAGAGGCAAGAGAACCTCAAAATGTTTATCG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 328 GAAACTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AAGTATAGGCGCGCAAGACTTTGACAAAGACATTTGGACCTGAGACTCCATATAT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 AAGTATATGCGCGCACAGATTATGATTCGACAGTGTGACCTGAGACTCCATATCT 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 CAGATCAAGGACAGGCGCTGTATCAATGTTTGTGATCATATTAAGGCGCAAGAGCTC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 448 CAGATCAAGGACAGGCGCTGTATCAATGTTTGTGATCATATTAAGGCGCAAGAGATG 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 568 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 ATACAGGTTATCCAGACCAAGAGATG 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 625 ATACAGGTTATCCAGACCAAGAGATG 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 3

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1001.13 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-19

Sequence: 1 atgatactcagatgcactat.....acacagactacacagattt 840

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
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6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hnc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_pln:*
15: em_gss_vitl:*
16: em_gss_vitl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	358	42.6	655	10	BI824940 603032554
3	323.8	38.5	448	9	AA056906 EST324R.P
4	281.4	33.5	629	9	BB631711 BB631711
5	263.2	31.3	1002	10	BF137460 BF137460
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ALIGNMENTS

RESULT 1
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DEFINITION 603063172P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212648 5',
BI906246
ACCESSION BI906246
VERSION BI906246.1 GI:16168907
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LILAM1533 row: 0 column: 17
High quality sequence stop: 719.
Location/Qualifiers
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/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6, Site_1: NotI; Site_2: EcoRV
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non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

FEATURES

source

Sun Oct 20 08:15:47 2002

us-09-646-561-19.rge

Page 11

Oy 658 CTGCACCTTGAAGTCATGAAAGCTTCCCTCCTCCCACTTAATATAATAGA 704
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Search completed: October 20, 2002, 03:16:11
Job time : 1156.19 secs

Best Local Similarity 80.5%; Pred. No. 8,7e-113;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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Db 664 CTGGAACCTGACAGAGAGCGGCTTTATCTTCTCCTTCTATATAGA 710
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RESULT 11
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LOCUS ARI60451 751 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 34 from patent US 6255073.
ACCESSION ARI60451
VERSION ARI60451.1 GI:16224368
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 751)
AUTHORS Cal, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6255073-A 34 03-JUL-2001;
FEATURES
source 1..751
location/Qualifiers
BASE COUNT 218 a 174 c 149 g 210 t
ORIGIN

Query Match 55.2%; Score 463.8; DB 6; Length 751;

Best Local Similarity 80.5%; Pred. No. 8,7e-113;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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Db 664 CTGGAACCTGACAGAGAGCGGCTTTATCTTCTCCTTCTATATAGA 710
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RESULT 12
ARI47736
LOCUS ARI47736 1002 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 33 from patent US 6225042.
ACCESSION ARI47736
VERSION ARI47736.1 GI:15111826
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Cal, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6225042-A 33 01-MAY-2001;
FEATURES
source 1..1002
location/Qualifiers
BASE COUNT 309 a 215 c 203 g 275 t
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LOCUS PIGCD86G 994 bp mRNA linear MAR 17-JUN-1997
DEFINITION Sus scrofa CD86 mRNA, complete cds.
ACCESSION L76099.1 GI:2198558
VERSION L76099.1 GI:2198558
KEYWORDS T cell costimulation.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Boher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and
Bohwell,A.L.
Porcine endothelial CD86 is a major costimulator of xenogeneic
human T cells: cloning, sequencing, and functional expression in
human endothelial cells
JOURNAL J. Immunol. 157 (9), 3838-3844 (1996)
MEDLINE 97047772
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Qy 79 AAGACTCAAGCATATTTCAACAGACTGAGAACTGCCATGCCATTTTACAAATTC 138
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Qy 499 CCCAAGAGATGATTTTGGTAAACCGAGATTTCAAGTCAAGTCAAGTCAAGTCA 558
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Qy 559 ATGAAGAAATTCGAAATATGATGATGATGATGATGATGATGATGATGATGATG 618
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Db 598 CCATCCCTCCCGAGCAAAATGAGCATCTTCTGCTGCTGCACTTGAATGAA- 657
Qy 678 -----GCTTCCCTCCCTACCTTATATAGAAACCA 710
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AX027016 994 bp DNA linear PAT 16-SEP-2000
LOCUS AX027016
DEFINITION Sequence 13 from Patent WO0037102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Rogers,N.J., Dorling,A. and Lechler,R.I.
Immunosuppression
Patent: WO 0037102-A 13 29-JUN-2000;
ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
LECHLER ROBERT IAN (GB)
JOURNAL
TITLE
AUTHORS
REFERENCE
FEATURES
location/Qualifiers
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ORIGIN
Query Match 57.6%; Score 484; DB 6; Length 994;

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SOURCE	Felis catus peripheral blood mononuclear cell cDNA to mRNA.		
ORGANISM	Felis catus		
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
AUTHORS	1 (sites)		
TITLE	Nishimura,Y., Shimojima,M., Miyazawa,T., Sato,E., Nakamura,K., Izumiyu,Y., Ikeda,Y., Mikami,T. and Takahashi,E.		
JOURNAL	Molecular cloning of the cDNAs encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA4-Ig		
MEDLINE	Enr. J. Immunogenet. 27 (5-6), 427-430 (2000)		
REFERENCE	20485322		
AUTHORS	2 (bases 1 to 1270)		
TITLE	Nishimura,Y.		
JOURNAL	Direct Submission		
	Submitted (31-JUL-1999) Yoshitiro Nishimura, Faculty of Agriculture, The University of Tokyo, Department of Veterinary Microbiology; 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan (E-mail:yoshitiro@crocos.ocn.ne.jp, Tel:+81-3-5841-5396, Fax:+81-3-5841-8184)		
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ORIGIN			
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QY	134 CTCAAAACATTAAGCCGAGATGAGTTGGTAGTGTGTTTGGCAGAGCAAGATTAAGCTG 193		
Db	376 CTCAAAACATTAAGCTGAGATGAGCTGTACTATTTTTGGCAGGACACAGATTAAGCTG 435		
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[illegible]

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RESULT 3
LOCUS   AF157827      1138 bp      mRNA      linear      MAM 08-MAY-2000
DEFINITION   Felis catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION   AF157827
VERSION     AF157827.1  GI:5381423
KEYWORDS
SOURCE     .
ORGANISM   cat.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1 (bases 1 to 1138)
AUTHORS    Choi,I.-S., Hash,S.M., Winslow,B.J. and Collisson,E.W.
TITLE      Sequence analyses of feline B7 costimulatory molecules
JOURNAL    Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE    20180222
PUBMED     10713336
REFERENCE   2 (bases 1 to 1138)
AUTHORS    Choi,I.-S., Hash,S., Winslow,B.J. and Collisson,E.W.
TITLE      Direct Submission
JOURNAL    Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
            University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA
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Best Local Similarity 89.4%; Pred. No. 2,5e-144;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
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QY      134  CTCGAAACATTAACCTCGAGTGGTGTGTTGGAGAGCCAGATTAAGCTGTTG 193
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RESULT 4
LOCUS     AB030652      1270 bp      mRNA      linear      MAM 01-MAR-2001
DEFINITION   Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86),
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RESULT 2
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
dog;
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1897)
Yang,S. and Sim,G.-K.
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
Immunogenetics 50 (5-6), 349-353 (1999)
20093996
MEDLINE
2 (bases 1 to 1897)
REFERENCE
Yang,S. and Sim,G.-K.
Direct Submission
Submitted (16-Nov-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
JOURNAL
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GenCore version 5.1.3
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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	704	83.8	1897	4	AF106826	Canis fam
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ALIGNMENTS

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AUTHORS
JOURNAL
MEDLINE
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AUTHORS
TITLE
JOURNAL
FEATURES

AF106827
Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.
AF106827.1 GI:6572518
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dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 1795)
Yang, S. and Sim, G.-K.
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
Immunogenetics 50 (5-6), 349-353 (1999)
20093996
2 (bases 1 to 1795)
Yang, S. and Sim, G.-K.
Direct Submission
Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
Location/Qualifiers

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Job time : 45.2281 secs

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; Sequence 226, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326.186B
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
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; TYPE: DNA
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US-09-326-186B-226

Query Match 57.88; Score 570.2; DB 4; Length 1424;
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Matches 767; Conservative 0; Mismatches 198; Indels 18; Gaps 6;

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Db 323 TGATAGGATATCTTAGGCAAAAGAAATTTGACAGTGTTCATTTCCAGTATATGGGCC 382
Qy 254 GCACAACTTTGACAAAGACAAATTTGACCTGAGCTCCATTAATATTCAGATCAAGACA 313
Db 383 GCACAACTTTGATTTGAGGACAGTTGAGACCTGAGACTTCAATCTTCAGATCAAGACA 442
Qy 314 AGGCTTGTATCATGTTTCTGTCATATTAAGGGCCCAAGAGCTGTTCCATGCAAC 373
Db 443 AGGCTTGTATCATGATATCATATCATATCAAAAAGCCACAGAGATGATTCGATCCACC 502
Qy 374 AGATGAATTTCTACCTATACAGTGTGCTAATCTTCACTGAGTCAACCTGAATATGTAAT 433
Db 503 AGATGAATTTCTAATCTGATGAGTGTGCTAATCTTCACTGAGTCAACCTGAATATGTAAT 562
Qy 434 CTATATGAACAGAAATTTCTGGCATATTAATTTGACCTGCTCATATCAATCAAGTTACC 493
Db 563 CTATATTAACAGAAA--TGTTGATCAATAATTTGACCTGCTCATATCAACAGTTACC 619
Qy 494 CAGAACCAAGAGATGATTTTGTGTAATAAACGAGAAATCAAGTACTAATAGTATGATA 553
Db 620 CAGAACCTTAAGAAAGATGAGTGTGTTGCTAAGAACCAAGAAATTCACATGAGTATGATG 679
Qy 554 CTGTCTATGAAGAAATCTCAAAATATATGTCAGAACTCTACAGCTTTCTATCAGCTTGT 613
Db 680 GTATTATGCAAAAATCTCAAGATATGTCAGAACTGTACAGAGTTCATCCATCAGCTTGT 739
Qy 614 CCTTCTACGTCCCTGAG--CAAGCAATGTGAGCATCTTGTGCTGCAACTTGTAGT 670
Db 740 CTGTTTCAATCCCTGATGTTAGAGCAATATGACCATCTTCTGTATTTCTGAAACTGACA 799
Qy 671 CAATGAAGTTCCCTCCCTACCTTATTAATATAGATCAATACGAACCAACCCCTGATG 730
Db 800 AGACGCGCTTTATCTTCACTTCTCTATAGA--GCTTGAAGAGCCCTGAGCCTCCC 856
Qy 731 GAGACCAATCTCTGATGATGGGCTGCTGTATGATGTTGCTATTTGGTGGAGTGG 790
Db 857 CAGACCAATCTCTTGGATTAACAGCTGATCTTCA--CAGTATTAATATGATGATGG 913
Qy 791 TGTCTTTCTAACAATAAGAAA--AGAGAAGAAAGACAGCTGCGCCCTCTCATGAT 847
Db 914 TTTTCTGTCTAATTTCTATGGAATGGAAGAAAGAAAGAGCGGCTCGCACTCTTATAAT 973
Qy 848 GTGAACCAACAAAGTGAAGAGAAAGAAAGTGAAGACCAAGAGAAAGTACAGTAC 907
Db 974 GTGGAACCAACCAATGAGAGAGAGAGAGTGAACAGACCAAGAGAAAGAAAGAAATTC 1033
Qy 908 ATGAACGGAAGATCTGATGAAGCCAGTGTG--TTAATATTTCAAGACAGCTTCAAG 964
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? APPLICANT: Nadler, Lee M.
? TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
? TITLE OF INVENTION: and Uses Therefor
? NUMBER OF SEQUENCES: 61
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 State Street, suite 510
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109-1875
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: ASCII text
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/205,697A
? FILING DATE: 02-Mar-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragoras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: BMI-120
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 24:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1161 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 148..1134
? US-08-205-697A-24

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Query Match      58.3%; Score 575.2; DB 4; Length 1161;
Best Local Similarity 77.8%; Pred. No. 1,7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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QY 1 ATGTATCTCAGATGCAATGAGTGAATGATTCCTCTTGATGAGACCCCTCCTC 60
DB 148 ATGGATCCCCAGTGCATGAGGAGTGAATCATCTCTTGATGAGCCCTCCTC 207
QY 61 TATGTGCTGCTTCATGATGAGTCAAGCATATTTCAACAAGACTGAGAACTGCATGC 120
DB 208 TCTGGTGTGCTCCTCTGATGAGATTCAGCTTATTTCAATGAGACTGCAGACTGCATGC 267
QY 121 CATTTTACAATTCACAAACATAAGCCTGGATGAGTGGTAGTGTGTTGGCAGAGCCAG 180
DB 268 CATTTTGAACAATCTCAAAACCAAGCCTGATGAGCTAGTAGTATTTGGCAGAGCCAG 327
QY 181 GATAAGCTGTTCTGTACGAGCTATACAGAGCAAGAAGAACCTCAAAATGTTCAATGC 240
DB 328 GAAAACTGTTCTGATGATGAGTATACCTTAGGCAAGAAGAAATTTGACAGTTCATTC 387
QY 241 AAGTATAGGGCGCCGACAAAGCTTTGACAAAGCAATTTGACCCCTGAGACTCCATAATTT 300
DB 388 AAGTATATGCGCGACAAAGTTTTATTCGGACAGTTGGACCCCTGAGACTTCACAATCTT 447
QY 301 CAGATCAAGGACAAAGGCTTTGATCAATGTTGCTTCATCAAAAGGCCCAAGGAGACTC 360
DB 448 CAGATCAAGGACAAAGGCTTTGATCAATGTTGCTTCATCAAAAGGCCCAAGGAGATG 507
QY 361 GTTCCCATGACCAAGATGATTTGACCTATTCAGTGTCTGTAACCTTCAGTCAACCTGAA 420
DB 508 ATTCCGATCCACCAATGATGATTTGACCTATTCAGTGTCTGTAACCTTCAGTCAACCTGAA 567
QY 421 ATTAATGTAATCTTAATTAAGACAAATATCTGGCATCATTAATTTGACCTGCTCAGCC 480
DB 568 ATATGATCCAAATTTTAATTAATTAAGACAAATATCTGGCATCATTAATTTGACCTGCTCAGCT 624

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QY 481 ATACAGGTTACCCAGAACCCAGAGATGTAATTTTGGTAAACCAGCAATTCAGT 540
DB 625 ATACAGGTTACCCAGAACCCAGAGATGTAATTTTGGTAAACCAGCAATTCAGT 684
QY 541 ACTAGTATGATGCTGATGAGAAATCTCAAAATATATGTCACAGAACTCTCAACGTT 600
DB 685 ATGAGTATGATGATGATGAGAAATCTCAAAATATATGTCACAGAACTCTCAACGTT 744
QY 601 TCTATCAGCTTCCCTCTCAGTCCCTGAAG--CAAGCAATGTAGACATCTTCTGTGTC 657
DB 745 TCCATCAGCTTCTCTGTTCAATTCCTGATGTATACAGACAAATATGACCATCTCTGTAT 804
QY 658 CAGCAACTGATCAATGATGAGTCCCTCCTACCTATATATATAGATGCAATAGCAAA 717
DB 805 CTGGAAGCTGACAGACGCGGCTTTATCTTCACCTCTCTATAGA---GCTTGAAGAC 861
QY 718 CCCACCCCTGATGAGACACATCTCTGATTTGCGGCTCTGCTTAATGTTGTCATT 777
DB 862 CCTCAGCCTCCCCAGACACATCTCTGATTTACAGCTGTACTTCCAA--CAGTTATT 918
QY 778 TTGTGAGATGCTGTTCTTCTAAGTAAAGAA--AGAGAAAGACCGCCTGCG 834
DB 919 ATATGATGATGTTTCTGCTTAATTTATGAAATGAAAGAAAGAGAGAGAGAGAGAGAG 978
QY 835 CCTCTCATGATGTGAACCAACAAAGTGAAGAAAGAAAGTGAAGACCAAGAA 894
DB 979 AACTCTTAATATGTAAGCAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 895 AGAGTACGTTACCATGAACCAAGCAAGATCTGATGAAGCCCGCTG--TTAATTTTCG 951
DB 1039 AGAGAAATATATGTAAGCAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 952 AAGACAGCTTCAGGCGACACAGTACTACAGATT 987
DB 1099 AAGACATCTTCAATGGCAGACAAAGTATGATGTTT 1134

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RESULT 13
US-08-702-525-24
? Sequence 24, Application US/08702525
? Patent No. 6294660
? GENERAL INFORMATION:
? APPLICANT: Sharpe, Sharpe
? APPLICANT: Borriello, Francescopaolo
? APPLICANT: Freeman, Gordon
? APPLICANT: Nadler, Lee
? TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
? NUMBER OF SEQUENCES: 65
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 28 State Street
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109-1875
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: ASCII text
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/702,525
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/205,697
? FILING DATE: 02-Mar-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragoras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: BMI-120CPUS
? TELECOMMUNICATION INFORMATION:

```

Db 821 CCTCAGCCTCCCCAGACCCACATCTCTTGATTTACAGCTTACTTCCAA---CAGTTATT 877
 QY 778 TTGTGGGATGGTGTCTTTCTTACACTAAGAAA--AGAAAGAGAGACGACCTGGC 834
 Db 878 ATATGTGTGATGGTTTCTGTCTAATTCATGTGAAATGGAAGAAGAACGCGCTCGC 937
 QY 835 CCCCTCATGATGTGAACCAACAAAGTGAAGAAAGAAAGTGAAGCAGACCAAGAA 894
 Db 938 AACCTTATTAATGTGGAAACCAACACAAATGAGAGAGAGTGAACAGACCAAGAA 997
 QY 895 AGAGTAGGACATGATGAAGAGATGATGAAGCCAGTGTG---TTAACAATTTG 951
 Db 998 AGAAGAAAATTCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGTGC 1057
 QY 952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
 Db 1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093

RESULT 11
 PCT-US95-02576-22
 ; Sequence 22, Application PC/TUS9502576
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 ; TITLE OF INVENTION: and Uses Therefor
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; City: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02576
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/205,697
 ; FILING DATE: 02-Mar-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: BWI-120CPPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1120 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 107..1093
 ; PCT-US95-02576-22

Query Match 58.3%; Score 575.2; DB 5; Length 1120;
 Best Local Similarity 77.8%; Pred. No. 1,7e-165;
 Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

QY 1 ATGATATCAAGATGCACTAGTGAACATATCTCTTTGTGAGACCTCTGCTC 60
 Db 107 ATGATATCAAGATGCACTAGTGAACATATCTCTTTGTGAGACCTCTGCTC 166

QY 61 TATGGNGCTGCTTCCATGAGAGTCAAGCATATTTCAACAGACTGGAGAACTCCATGC 120
 Db 167 TCTGGTGTGCTGCTCTCTGTAAGATTTAAGCTTATTTCAATGAGACTGCGACCTGCAATGC 226
 QY 121 CATTTTACAAATTTCTCAAAACATAGCCTGATGAGTGTGATGTTTGGCAGACCAAG 180
 Db 227 CAATTTGCAAACTCCAAACCAACCAAGCCTGAGTGAAGTATGATTTTGGCAGACCAAG 286
 QY 181 GATAAGCTGTGTTCTAGAGAGTATACAGAGCAAGAAAGAAAGCCCAAAATGTCATGCC 240
 Db 287 GAAACCTGTTCTGTAATGAGATATCTTAGGCAAGAAAGAAATTTGACAGTGTTCATTC 346
 QY 241 AAGTATTAAGGCGCGCAACAAGCTTTGACAAAGCAATTTGACCTGAGACTCATATATTT 300
 Db 347 AAGTATTAAGGCGCGCAACAAGCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 406
 QY 301 CAGATCAAGAGCAAGAGGCTTTGATATCAATGTTTCCATCATTAAGGCCCCAAGGATC 360
 Db 407 CAGATCAAGAGCAAGAGGCTTTGATATCAATGATCATCATCAACAAAAGCCCAAGGAATG 466
 QY 361 GTTCCCATGCGCAGATGATGATTCAGCTATGAGTGTGCTTCACTTCACTGATCAACCTGAA 420
 Db 467 ATTCCCATGCGCAGATGATGATTCAGCTATGAGTGTGCTTCACTTCACTGATCAACCTGAA 526
 QY 421 ATAATGTAACCTTCTAATAGAAACAGAAAATTCGSCATCATTAATTTGACCTGCTCATCC 480
 Db 527 ATAGTACCAATTTCTAATATTAACAGAAA---TGTTACATTAATTTGACCTGCTCATCT 583
 QY 481 ATACAAGTGTACCGAAGAACCCAGAGAGATGATTTTGGTATTAATTAATTAATTAATTAAT 540
 Db 584 ATACAGGTTTACCGAAGAACCCAGAGAGATGATGTTTGGTATTAATTAATTAATTAATTAAT 643
 QY 541 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Db 644 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
 QY 601 TCTATGAGCTTGTCTTCTTCACTGCTGAG---CAAGCAATGAGCATCTTCTGTGC 657
 Db 704 TCCATGAGCTTGTCTTCTTCACTGCTGAG---CAAGCAATGAGCATCTTCTGTGT 763
 QY 658 CTGCACTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 717
 Db 764 CTGGAACCTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 820
 QY 718 CCCACCCCTGATGAGCAACATCTCTGATGAGGCTCTGCTGTAATGTTGTCATTT 777
 Db 821 CCTCAGCCTCCCCAGACCCACATCTCTTGATTTACAGCTTACTTCCAA---CAGTTATT 877
 QY 778 TTGTGGGATGGTGTCTTTCTTACACTAAGAAA--AGAAAGAGAGACGACCTGGC 834
 Db 878 ATATGTGTGATGGTTTCTGTCTAATTCATGTGAAATGGAAGAAGAACGCGCTCGC 937
 QY 835 CCCCTCATGATGTGAACCAACAAAGTGAAGAAAGAAAGTGAAGCAGACCAAGAA 894
 Db 938 AACCTTATTAATGTGGAAACCAACACAAATGAGAGAGTGAACAGACCAAGAA 997
 QY 895 AGAGTAGGACATGATGAAGAGATGATGAAGCCAGTGTG---TTAACAATTTG 951
 Db 998 AGAAGAAAATTCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGTGC 1057
 QY 952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
 Db 1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093

RESULT 12
 US-08-205-697A-24
 ; Sequence 24, Application US/08205697A
 ; Patent No. 6218510
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharpe, Arlene H.
 ; APPLICANT: Borriello, Francescopaulo
 ; APPLICANT: Freeman, Gordon J.

Db 704 TCCATCAGCTTCTGTTTCATTCCTGATGTAGAGCAATATACCATCTTCTGTATT 763
QY 658 CTGCAACTTGAGTCATGAAAGCTTCCCTCCACCTTATTAATATGATGACATACGAAA 717
Db 764 CTGGAACATGACAAAGCGGGCTTTATCTTACCTTCTCTATAGA---GCTTAGAGAC 820
QY 718 CCCACCCCTGATGAGAACCAATCTCTGATTTGGGGCTGCTGTATGTTGGTCAAT 777
Db 821 CCTCAGCCCTCCCAACACATCTCTGATTTACAGCTTACCTTCCAA---CACTTATT 877
QY 778 TTGTGGGATGTTCTTCTTCTTACACTAGAAA---AGAGAGAGAGACGCTGGC 834
Db 878 ATATGCTGATGTTCTTCTTCTTATGTAATGGAATGGAAGAAAGAGAGCGGCTCGC 937
QY 835 CCCCTCATGATGTGAACCAACAAAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 894
Db 938 AACTCTTAAATGTGGAACCAACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 997
QY 895 AGAGTACGCTACATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 951
Db 998 AGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCGAGCTTTTAAAGTTGC 1057
QY 952 AAGACAGCTTACGCGGAGCAACAGTACTACAGATT 987
Db 1058 AAGACATCTTCTGCGCAAAAGTATACATGTTT 1093

RESULT 10
US-08-403-253A-3
Sequence 3, Application US/08403253A
Patent No. 6352694

GENERAL INFORMATION:

APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennett, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08403,253A
FILING DATE: March 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433

FILING DATE: 23 NOV 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-403-253A-3

Query Match 58.3%; Score 575.2; DB 4; Length 1120;
Best Local Similarity 77.8%; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

QY 1 ATGTATCTCATGATGCACTATGAGCAATTAATCATTTCTTTGTGATGACCCCTGCTGC 60
Db 107 ATGATGCCAGTGCAGTACTATGAGCACTGATGATTTCTTTGTGATGACCTTCTGCTC 166
QY 61 TATGTGCTGCTTCCATGAGAGTCAAGCATTTTCAACAGACTGAGAGACTGCCATGC 120
Db 167 TCTGTGCTGCTCCTCTGAAATTCAGCTTATTTCAATGAGACTGACAGACCTGCCATGC 226
QY 121 CATTTACAAATTCGAAAACATAAGCTGGATGATGATGTTGTTGTTGGAGAGCCAG 180
Db 227 CAATTTGCAACTCTTAACCAACCAAGCTGAGTGTATGTTTGGAGAGCCAG 286
QY 181 GATAAGCTGTTCTGTAGCAGTATACAGAGGCAAGAGAACCTCAAAATGTTGATGCG 240
Db 287 GAAACCTGTTCTGTAATGAGTATCTAGGCAAGAAATTTGACAGTGTTCATTC 346
QY 241 AAGTATAGGGCCGCGCAAGCTTTGCAAGAACATTTGACCTGAGACTCCATATATT 300
Db 347 AAGTATAGGGCCGCGCAAGCTTTGCAAGAACATTTGACCTGAGACTCCATATATT 406
QY 301 CAGATCAAGAGCAAGGGCTTTGATCATGTTTCTGTTCAATTAAGGGCCCAAGAGCTC 360
Db 407 CAGATCAAGAGCAAGGGCTTTGATCATGTTTCTGTTCAATTAAGGGCCCAAGAGAG 466
QY 361 GTTCCATGCAACCAAGTATTTGACCTATGACGTGTTGTTGTTGTTGTTGTTGTTGTT 420
Db 467 ATTGCGATCCACCAAGTATTTGACCTATGACGTGTTGTTGTTGTTGTTGTTGTTGTT 526
QY 421 ATATAGTACTTCTTAATGAGACAGAAAATTTGCGATCATTAATTTGACCTGCTATCC 480
Db 527 ATATAGTACTTCTTAATGAGACAGAAAATTTGCGATCATTAATTTGACCTGCTATCC 583
QY 481 ATACAGGTTTACCAAGAACCCCAAGAGATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 540
Db 584 ATACAGGTTTACCAAGAACCCCAAGAGATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 643
QY 541 ACTAAGTATGATCTGATGAGAAATCTCAAAATTAATGTCACAGAACTGACAACTG 600
Db 644 ATGAGTATGATGTTATGAGAAATCTCAAAATTAATGTCACAGAACTGACAACTG 703
QY 601 TGTATCAGTTGTTCTTCTGAGTCCCTGAG---CAACATGAGAGATTTCTGTGTC 657
Db 704 TGTATCAGTTGTTCTTCTGAGTCCCTGAGTATGAGAAATTAATGTCACAACTGTTGTT 763
QY 658 CTGCAACTTGAGTCATGAAAGCTTCCCTCCACCTTATTAATATGATGACATACGAAA 717
Db 764 CTGGAACATGACAAAGCGGGCTTTATCTTACCTTCTCTATAGA---GCTTAGAGAC 820
QY 718 CCCACCCCTGATGAGAACCAATCTCTGATTTGGGGCTGCTGTATGTTGGTCAAT 777

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-280-757B-1

Query Match 58.38; Score 575.2; DB 3; Length 1120;
Best Local Similarity 77.88; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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QY 1 ATGTATCTCAATGACATATGAACTGAATACATCTCTTTGTGATGACCTCTGCTC 60
DB 107 ATGATATCCCACTGACATATGAGTAACTCTCTTTGTGATGAGCTCTGCTC 166
QY 61 TATGTCGTCCTTCATTAAGATCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
DB 167 TCTGTCGTCCTTCATTAAGATCAAGCTTATTTCAATGAGCTGAGACCTGCCATGC 226
QY 121 CATTTTAAATTTCAAAACATTAAGCTTGATGATGTTGTGATGTTGGCAGACAG 180
DB 227 CATTTTGAATCTCAAAACCAAGCCTGATGAGTATGATTTTGGCAGACAG 286
QY 181 GATAAGCTGTTCTGTACAGACTATACAGAGCAAGAACCTCAAAATGTTCAATCC 240
DB 287 GAAACCTGTTCTGAAATGAGTATCTTACGCAAGAAATTTGACAGTGTTCATTC 346
QY 241 AAGTATAGGGCCGACAAAGCTTTGACAAAGCAATTTGAGACCTGACACTCAATAT 300
DB 347 AAGTATAGGGCCGACAAAGCTTTGATTTGACAGCTTTGACACTCAATATCTT 406
QY 301 CAGATCAAGCAAGAGGCTTATCATATGTTGTTCAATTAAGAGCCCAAGACATC 360
DB 407 CAGATCAAGCAAGAGGCTTATCATATGTTCAATTAAGAGCCCAAGACATG 466
QY 361 GTTCCAGCAAGCAAGATTTGACATGACATGCTGTTGATCTCAGTCAACCTGAA 420
DB 467 ATTCCATCCACAGATTAATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 526
QY 421 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCC 480
DB 527 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCT 583
QY 481 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCT 540
DB 584 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCT 643
QY 541 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCT 600
DB 644 ATATGTTGTTCTTATTAAGCAAGAAATTTGTCATTAATTTGACCTGCTCATCT 703
QY 601 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
DB 704 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
QY 764 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
DB 821 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
QY 877 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
DB 934 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
QY 997 TCTATCAGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057

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QY 952 AAGACAGCTTGACGACCAACAGTACTACACAGTTT 987
DB 1058 AAGACATCTCATGCGACAAAGATGATACATGTTT 1093

RESULT 8
US-08-205-697A-22
Sequence 22, Application US/08205697A
Patent No. 6218510

GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.

APPLICANT: Borriello, Francescopaulo

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,697A

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandiagouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BMI-120

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 1120 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 107..1093

US-08-205-697A-22

Query Match 58.38; Score 575.2; DB 4; Length 1120;

Best Local Similarity 77.88; Pred. No. 1.7e-165;

Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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QY 1 ATGTATCTCAATGACATATGAACTGAATACATCTCTTTGTGATGACCTCTGCTC 60
DB 107 ATGATATCCCACTGACATATGAGTAACTCTCTTTGTGATGAGCTCTGCTC 166
QY 61 TATGTCGTCCTTCATTAAGATCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
DB 167 TCTGTCGTCCTTCATTAAGATCAAGCTTATTTCAATGAGCTGAGACCTGCCATGC 226
QY 121 CATTTTAAATTTCAAAACATTAAGCTTGATGATGTTGTGATGTTGGCAGACAG 180
DB 227 CATTTTGAATCTCAAAACCAAGCCTGATGAGTATGATTTTGGCAGACAG 286
QY 181 GATAAGCTGTTCTGTACAGCTATACAGAGCAAGAACCTCAAAATGTTCAATCC 240
DB 287 GAAACCTGTTCTGAAATGAGTATCTTACGCAAGAAATTTGACAGTGTTCATTC 346
QY 241 AAGTATAGGGCCGACCAAGCTTTGACAAAGCAATTTGAGACCTGACACTCAATAT 300

```


APPLICANT: Nadler, Lee M.
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/101,624
 FILING DATE: 26-JUL-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1120 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 107..1093
 US-08-101-624-1

Query Match 58.3%; Score 575.2; DB 2; Length 1120;
 Best Local Similarity 77.8%; Pred. No. 1,7e-165;
 Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;
 QY 1 ATGTATCTCAGATGCACTATGGAATCTGTAATCAATTCCTTTGTGATGACCCCTGCTC 60
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 QY 61 TATGCTGCTCTTCATGAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCATGC 120
 Db 167 TCTGGTGCCTCTCTGTAAGATTCACCTTATTTCAATGAGACTGCAGACCTCCATGC 226
 QY 121 CATTTACAAATTTCAAAAACATAGCCTGATGAGTGGTGTAGTGTGTTGGCAGACAG 180
 Db 227 CAATTTGCAAACTCTCAAAAACAAAGCCTGAGTGAAGTATTTTGGCAGACAG 286
 QY 181 GATTAAGCTGGTCTGTACAGCTATACAGAGGCAAGAAACCTCAAAATGTTCAATGC 240
 Db 287 GAAACCTTGTCTCAATGAGGTATATAGGCAAGAAATTTGACAGTGTCAATTC 346
 QY 241 AAGTAAAGGGCGCACAAAGCTTTGACAAAGACATTTGGACCCGAGAGCTCATATATTT 300
 Db 347 AAGTAAAGGGCGCACAAAGCTTTTATTTGAGCAAGTTGGACCCGAGAGCTCATATATTT 406
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 Db 407 CAGATCAAGAGAGAGGCTTGTATCAATGATCATCAACAAAAGCCCAAGAGATG 466
 QY 361 GTTCCATGACCAAGATGAATTCAGCTATACAGTGTGTTAATCTTACGACCAAGCTGAA 420

Db 467 ATTGCATCCACAGATGATATTTCTGAATGTCAGTGCCTGCTACTTCACTCAACCTGAA 526
 QY 421 ATAATGTAATCTCTAATAGAACAAAATTTGGCATTCATTAATTTGACCTGCTATCC 480
 Db 527 ATAGTACAAATTTCTAATATACAGAAAA--TGTGTACATTAATTTGACCTGCTATCT 583
 QY 481 ATACAGGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAAGAGATTCAGT 540
 Db 584 ATACAGGTTACCCAGAACCTTAAGAGATGAGTGTTTTGGCTAAGAACCAAGAAATTCAC 643
 QY 541 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTACAGAACTCTACAGCTT 600
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 QY 718 CCCACCCCTGATGAGACCAATCTCTGATTCGGCTGCTGTTGATGTGTGAT 777
 Db 821 CCTCAGCCTCCCGACAGACCATTCCTTGATTCAGCTGTACTCCAA--CAGTTAT 877
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 Db 1058 AAGACATCTTCATGCGACAAAAGTATCAATGTTTT 1093

RESULT 6
 US-08-479-744A-1
 Sequence 1, Application US/08479744A
 Patent No. 6084067
 GENERAL INFORMATION:
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/479,744A
 FILING DATE: June 7, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/280,757
 FILING DATE: 26-JUL-1994

Oy	778	TTTGTTGGGATGAGGTTCTTTCTTAACACTAAGGAAA---AGGAAAGAAAGACGACCGC	834
Db	778	ATATCTGGAGGGTTTCTTGCTATTTCTATGAGAAATGGAAGAAAGAAAGCGCCTCGC	837
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Db	838	AACTCTTTTAATGTGGAGAACCAACAAATGGAGAGGGAAGAGATGACAGACCAAGAA	897
Oy	895	AGAGTACGGTCCATGAAACGGAAAGATCTGATGACCCACAGTGTG---TTAACATTTTCG	951
Db	898	AGAGAAAAAATCCATATACCTGGAAGAGATCGATGCAACCCAGCGGTGTTTAAAGATTGC	957
Oy	952	AAGACAGCTTCAGGCGCAACAGTACATACACAGTTT	987
Db	958	AAGACATTTTCATGCGACCAAGAGATACATCTTTT	993

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1      RESULT 4
2      US-08-456-104-1
3      ; Sequence 1, Application US/08456104
4      ; Patent No. 5861310
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Freeman, Gordon J.
7      ; APPLICANT: Nadler, Lee M.
8      ; APPLICANT: Gray, Gary S.
9      ; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
10     ; NUMBER OF SEQUENCES: 8
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: LAHIVE & COCKFIELD
13     ; STREET: 60 State Street, Suite 510
14     ; City: Boston
15     ; STATE: Massachusetts
16     ; COUNTRY: USA
17     ; ZIP: 02109
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/456,104
25     ; FILING DATE:
26     ; CLASSIFICATION: 424
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: 08/101,624;
29     ; FILING DATE: 26-JUL-1993;
30     ; APPLICATION NUMBER: 08/109,393;
31     ; APPLICATION NUMBER: 19-AUG-1993
32     ; ATTORNEY/AGENT INFORMATION:
33     ; NAME: Mandragouras, Amy E.
34     ; REGISTRATION NUMBER: 36,207
35     ; REFERENCE/DOCKET NUMBER: RPI-008
36     ; TELECOMMUNICATION INFORMATION:
37     ; TELEPHONE: (617) 227-7400
38     ; TELEFAX: (617) 227-5941
39     ; INFORMATION FOR SEQ ID NO: 1:
40     ; SEQUENCE CHARACTERISTICS:
41     ; LENGTH: 1120 base pairs
42     ; TYPE: nucleic acid
43     ; STRANDEDNESS: single
44     ; TOPOLOGY: linear
45     ; MOLECULE TYPE: cDNA
46     ; FEATURE:
47     ; NAME/KEY: CDS
48     ; LOCATION: 107..1093
49     ; US-08-456-104-1

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Query Match	58.3%	Score 575.2;	DB 2;	Length 1120;
Best Local Similarity	77.8%;	Pred. No. 1.7e-165;		
Matches 775; Conservative	0;	Mismatches 203;	Indels 18;	Gaps 6;
OY	1	ATGTCATCGACATGCACATATGCACTGAATTAACATTCTTTGTGTATGACCCCTCCTGCNC	60	

Db	107	ATGATGCCCCAGTGCACATATATGGAGTACGAGAACATCTCTTTGATGGACCTCTCCTGCTC	166
Oy	61	TATGGTGTCTGCTTCATGGAAGAGTCAAGCATATTTCAACAACACTGGAACTGGCAATGC	120
Db	167	TCTGGTCTGTCTCTCGAAGATTCAGCAAGCTTATATTCATAAGACATGCAAGCTGGCAATGC	226
Oy	121	CATTTCACAAATTCCTCAAAACATAGCTGGATGAGTTGGTGGTGGTTGGGAGAGCAG	180
Db	227	CAATTTGCAAACTCTCAAAACCCAAAGCCTGAGTGGCTGTGTATTTTGGGAGGACAG	286
Oy	181	GATAAGCTGTTTGTGTACGAGTATACAGAGGCAAGAGAACCTTCAAAATGTTTCATCGC	240
Db	287	GAACAATGGTTTGTGAATGAGTATACTTAAGGCAAGAAATTTGACAGTGTTCATTC	346
Oy	241	AAGTATTAAGGGCCGACACACCTTTGACAAAGACAAATTTGACCCCTGAGACTCATATAT	300
Db	347	AAGTATATGGGCCCCACAAATTTTGTGATGCGACAGTTGGACCTGAGATTCACACTTT	406
Oy	301	CAGATCAAGGACAGGGCCTTGATCATATGTTTGTCATCATATAAGGGGCCAAAGAGCTC	360
Db	407	CAGATCAAGGACAGGGCCTTGATCATATGTTTGTCATCATATAAGGGGCCACAGAGATG	466
Oy	361	GTTCCCATGACACAGATGAATTCGTGACCTATCAGTGCCTTCTAACTCAGTCAACCTGAA	420
Db	467	ATTGCATCCACAGATGAATTCGTGACCTGTCAGTGCCTTCTAACTCAGTCAACCTGAA	526
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Db	527	ATAGTACCAATTTTAAATATATACAGAAA--TGTCATCATAAATTTGACCTGGCTCATCT	583
Oy	481	ATACAGGTTATCCCGACAGACCAGAGAGATGTATTTTGGTATAAACCCAGAAATTCAGT	540
Db	584	ATACAGGTTATCCCGACAGAACCTAAGAAATGATGATGTTTGGTAAAGCAAGAAATTCAGT	643
Oy	541	ACTAAGTATGATCTGTCTATGAGAGAAATCTCAAAATATATGTACAGAACTCTACACGTT	600
Db	644	ATCGATGTGATGTTATATATGACAAATCTCAAGATAATGTCAAGAACTGTACAGCGTT	703
Oy	601	TCTATCAGCTGTCTCTTCAGTCCGAGG--CAAGCAATGTGACATCTTCTGTGTC	657
Db	704	TCTATCAGCTGTCTCTGTTCATCTCCGTGATTTACAGCAATATGACCATCTTCTGTAT	763
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Db	764	CTGCACACTTGATCAAGAGCGGCTTTATCTTCAACCTTCTCTATATA--GGTTGAGGAC	820
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Db	821	CCTCAGCTCCCCGACAGCAACATCTCTGGATTTACAGCTGTACTCTCCAA--CAGTAT	877
Oy	778	TGTGTGGGATGATGTTCTTCTTAACCTAAGAAA--AGSAAAGSAAAGGACGCTGGC	834
Db	878	ATATGTGTGATGTTTCTGTCTAATCTTATGAAAGAGSAAAGSAAAGAGGCGCTGCG	937
Oy	835	CCCTCTCATGATGTGAAGAACCAAAAGTGGAGAGAAACAAAGTGGAGAGACCAAGAA	894
Db	938	AACCTTTTAAATGTGGAGACCAACATGTGAGAGSAAAGSAAAGTGAACAGACCAAGAA	997
Oy	895	AGAGTACGATCATGAACGGAAGATCTGATGAAGCCCAAGTGTG--TTAACATTTGC	951
Db	998	AGAGAAAAATTCATATACCTGGAAGATGTGATGAAGCCCAAGCGTGTTTTAAAGTTGC	1057
Oy	952	AAGACAGCTTCAAGCGGACACACAGTACTACACAGTTT	987
Db	1058	AAGACATCTTCAATGCGACAAAGATATGATGTTT	1093

RESULT 5
US-08-101-624-1
; Sequence 1, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.

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Db 367 ATTGCATCCACACATGATTTCTAAGTCTGCTGCTAAGTCAACCTGAA 426
Oy 421 ATAATGTAAGTCTTAATAGAAACAGAAAAATCTGGCATCAATAATTGACCTGCATCC 480
Db 427 ATAGTACCAATTTCTAATATATACAGAAAA---TGTTGATCAATAAATTTGACCTGCATCT 483
Oy 481 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTTTGGTAAAAACCGAGATCAAGT 540
Db 484 ATACAGGTTACCCAGAAACCTAAGAGATGAGTGTGTTGCTAAGAACCAAGAAATCAACT 543
Oy 541 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATGTCAGAGCTTACAGAGTT 600
Db 544 ATCGAGTATGATGATATATGAGAAATCTCAAGTAAATGTCACAGAGCTTACAGAGTT 603
Oy 601 TCTATCAGCTGTCTCTCTCTGAGTCCCTGAAG---CAAGCAATGTGAGCATCTCTGTGTC 657
Db 604 TCCATCAGCTGTCTCTCTCTGATCTGATGATGAGCAATATGACCATCTCTGATTT 663
Oy 658 CTGCAACTTGAAGTCAATGAGTCCCTGCTACCTTATATATAGATGACATACGAAA 717
Db 664 CTGGAAGTGAACAGACGCGCTTTATCTTCACCTTTCTCTATAGA---GCTTGAGGAC 720
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Db 721 CCTGAGCCTCCCGACAGACACATCTCTGATGAGTACAGTACTTCCAA---CAGTTATTT 777
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Db 778 ATATGTGATGATGTTTCTGTTCTAATTTCTATGAAATGGAAGAGAAAGACGCTGCG 837
Oy 835 CCTCTCTGATGATGGAACCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
Db 838 AACCTTTAATATGATGAGACCAACACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897
Oy 895 AGAGTACGCTACATGGAACCGGAAGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
Db 898 AGAGAAAAATTCATATACCTGGAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
Oy 952 AAGACAGTTGAGCGGACACAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
Db 958 AAGACATCTTCATGCGACAAAAAGTATACATGTTT 993

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RESULT 3
 US-09-039-762A-33
 Sequence 33: Application US/09039762A
 Patent No. 6255073
 GENERAL INFORMATION:
 APPLICANT: Cai, Zeling
 APPLICANT: Sprent, Jonathan
 APPLICANT: Brunmark, Anders
 APPLICANT: Jackson, Michael
 APPLICANT: Peterson, Per A.
 TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
 TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Olson & Hiernl, Ltd.
 STREET: 20 No. 6255073th Wacker Drive, 36th Floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/039,762A
 FILING DATE: 16-MAR-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

```

? NAME: OLSON, Arne M.
? REGISTRATION NUMBER: 30,203
? REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 580-1180
? TELEFAX: (312) 580-1189
? INFORMATION FOR SEQ ID NO: 33:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1002 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? US-09-039-762A-33

Query Match 58.3%; Score 575.2; DB 4; Length 1002;
Best Local Similarity 77.8%; Pred. No. 1,6e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

Oy 1 ATGATCTGAGTACGACTATGAACTGAATTAACATTTCTTTGTATGACCTCTGCTC 60
Db 7 ATGATCTCCAGTGCACATGAGAGTGAATCAATTTCTTTGTATGAGCTTCTGCTC 66
Oy 61 TATGCTGCTGCTTCACAGAGAGTCAAGCATATTTCAACAGACCTGAGAGAGCTGATC 120
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Oy 241 AAGTATAGAGGCGCGACAGAGCTTTGACAAAGCAATTTGAGCCCTGAGACTCATATAT 300
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Oy 301 CAGATCAAGGACAGAGGCTTTGATCAATGTTTCTCATCAATTAAGAGGCGCAAGAGCTC 360
Db 307 CAGATCAAGGACAGAGGCTTTGATCAATGTTTCTCATCAATTAAGAGGCGCAAGAGT 366
Oy 361 GTTCCATGACACAGATGATTTCTGACCTATGAGAGCTTGTCAATTTCACTGATCACT 420
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Oy 601 TCTATCAGCTGTCTCTCTCTGAGTCCCTGAAG---CAAGCAATGTGAGCATCTCTGTGTC 657
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QY 1 ATGTATTCAGATGACACTATGGAAGTGAATACATCTCTTTGTGATGACCCCTCGCTC 60
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QY 301 CAGATCAAGCAAGGCTGATGAGTGAATATTCATGATGATGAGGCGCAAGGACTC 360
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DB 367 ATTGCGATCCAGAGATGATTTGAACTGCTGATGCTGCTGCTGCTGCTGCTGAA 426
QY 421 ATATGCTATCTTATGATGAGCAAAATTTGCGATCATTAATTTGACCTGCTATCC 480
DB 427 ATAGTACCAATTTCTATATATACAGAAA--TGTGTACTTAATTTGACCTGCTATCC 483
QY 481 ATCAAGTATCCAGCAAGGCTGATGAGTGAATTTTGTGTAAGGCGCAAGGACTCA 540
DB 484 ATCAAGTATCCAGCAAGGCTGATGAGTGAATTTTGTGTAAGGCGCAAGGACTCA 543
QY 541 ACTAAGTATGATGATGATGAGCAAAATTCGAAATATGATGATGATGATGATGAT 600
DB 544 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
QY 601 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
DB 604 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 658 CTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
DB 664 CTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 718 CCAACCTGATGAGAGCAACATCTGCTGATGAGGCTGCTGCTGATGATGATGAT 777
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QY 778 TTTGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
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DB 838 CCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
QY 895 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
DB 898 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
QY 952 AAGACAGCTTCAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 987
DB 958 AAGACAGCTTCAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 993

RESULT 2
US-09-039-641-33
; Sequence 33, Application US/09039641
; Patent No. 6251627

GENERAL INFORMATION:
APPLICANT: Cai, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6251627th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039, 641
FILING DATE: 8-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-641-33
Query Match 58.3%; Score 575.2; DB 4; Length 1002;
Best Local Similarity 77.8%; Pred. No. 1,6e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;
QY 1 ATGTATTCAGATGACACTATGGAAGTGAATACATCTCTTTGTGATGACCCCTCGCTC 60
DB 7 ATGTATTCAGATGACACTATGGAAGTGAATACATCTCTTTGTGATGACCCCTCGCTC 66
QY 61 TATGTGCTGCTTCATGGAAGTGAATATTCACAAAGTGGAGACTGGCATGC 120
DB 67 TCGGTGCTGCTTCATGGAAGTGAATATTCACAAAGTGGAGACTGGCATGC 126
QY 121 CATTTTACAATTTCTCAAAACATTAAGCTTGATGAGTGTGTGTTGGAGACG 180
DB 127 CAATTTGCAAACTCTCAAAACATTAAGCTTGATGAGTGTGTGTTGGAGACG 186
QY 181 GATAGAGCTGCTGATGAGTGAATACAGAGCAAGAGAACCTTCAATATGTCATCC 240
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QY 241 AAGTATTAAGGCGGCAAGGCTTTGACAAAGACATTTGACCTGAGCTCATATAT 300
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QY 361 GTTCCATGACCAAGATGAATTCGACCTATCATGCTTGTAACTTCACTCACTGAA 420

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 34.2281 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-9

Perfect score: 987
Sequence: 1 atgatactcagatgcactat.....acaacagtlactacacagttt 987

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.2	58.3	1002	4	US-09-039-982A-33
2	575.2	58.3	1002	4	US-09-039-641-33
3	575.2	58.3	1002	4	US-09-039-762A-33
4	575.2	58.3	1120	2	US-08-456-104-1
5	575.2	58.3	1120	2	US-08-101-624-1
6	575.2	58.3	1120	3	US-08-479-744A-1
7	575.2	58.3	1120	3	US-08-280-757B-1
8	575.2	58.3	1120	4	US-08-205-697A-22
9	575.2	58.3	1120	4	US-08-702-525-22
10	575.2	58.3	1120	4	US-08-403-253A-3
11	575.2	58.3	1120	5	PCR-US95-02576-22
12	575.2	58.3	1161	4	US-08-205-697A-24
13	575.2	58.3	1161	4	US-08-702-525-24
14	575.2	58.3	1161	5	PCR-US95-02576-24
15	570.2	57.8	1424	4	US-09-326-186B-226
16	570.2	57.8	1428	4	PCR-US94-09642-1
17	565.2	57.3	972	4	US-08-848-760B-11
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19	463.8	47.0	751	4	US-09-039-641-34
20	463.8	47.0	751	4	US-09-039-762A-34
21	344.4	34.9	1151	2	US-08-456-104-3
22	344.4	34.9	1151	4	US-08-205-697A-20
23	344.4	34.9	1151	4	US-08-702-525-20
24	344.4	34.9	1151	5	PCR-US95-02576-20
25	344.4	34.9	1163	3	US-08-479-744A-22
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27	337.2	34.2	1261	4	US-08-205-697A-12

28	337.2	34.2	1261	4	US-08-702-525-12	Sequence 12, Appl
29	337.2	34.2	1261	5	PCR-US95-02576-12	Sequence 12, Appl
30	232.4	23.5	1360	3	US-08-479-744A-44	Sequence 44, Appl
31	232.4	23.5	1360	3	US-08-280-757B-44	Sequence 44, Appl
32	175.2	17.8	306	3	US-08-479-744A-46	Sequence 46, Appl
33	175.2	17.8	306	3	US-08-280-757B-46	Sequence 46, Appl
34	103.4	10.5	210	4	US-08-205-697A-31	Sequence 31, Appl
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36	103.4	10.5	210	5	PCR-US95-02576-31	Sequence 31, Appl
37	45	4.6	195	4	US-08-205-697A-41	Sequence 41, Appl
38	45	4.6	195	4	US-08-702-525-41	Sequence 41, Appl
39	45	4.6	195	5	PCR-US95-02576-41	Sequence 41, Appl
40	39.4	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
41	34.6	3.5	492	2	US-08-874-347-1	Sequence 335, App
42	32.6	3.3	2747	2	US-08-874-347-1	Sequence 1, Appl1
43	32.6	3.3	2747	2	US-09-093-522-1	Sequence 1, Appl1
44	32.4	3.3	3341	2	US-08-868-577-18	Sequence 18, Appl1
45	32.2	3.3	6216	4	US-09-415-522-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-039-982A-33
Sequence 33, Application US/09039982A
Patent No. 6225042
GENERAL INFORMATION:
APPLICANT: Cal, Zelig
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6225042th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
US-09-039-982A-33

Query Match 58.3%; Score 575.2; DB 4; Length 1002;
Best Local Similarity 77.8%; Pred. No. 1.6e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;


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Db 924 GCAGAGTCCAT-----GAACGATCTGATGATGCCCACTGATGTTAATATTTTAAAG 977
QY 955 ACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
Db 978 ACAGCCTCAGATGACACACAGTACTACAGATTTT 1010
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Search completed: October 19, 2002, 23:33:08
Job time : 157.413 secs

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 Db 1189 TCTATCAGCTGTCTCTCTCAGTCCCTGAGCAAGCAATGTGAGCATCTCTGTGCTCG 1130
 Qy 661 CAACCTGATGATTAACCTTCCCTCCTACCTTATATATAGATGACATTA 712
 Db 1129 CAACCTGATGATTAACCTTCCCTCCTACCTTATATATAGAAACCAACA 1078
 RESULT 15
 ID AAA49661
 AC AAA49661 standard; cDNA: 1050 BP.
 AC AAA49661;
 DT 25-SEP-2000 (first entry)
 XX Pig costimulatory molecule CD86 (B7-2) cDNA.
 DE Pig costimulatory molecule CD86 (B7-2) cDNA.
 KM Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
 KM xerotransplantation; organ transplant; vaccine; ss.
 OS Sus scrofa.
 FH Key Location/Qualifiers
 FT CDS 36..1013
 FT /*tag= a
 XX W0200037102-A2.
 PD 29-JUN-2000.
 XX 17-DEC-1999; 99WO-GB04200.
 PF 19-DEC-1998; 98GB-0027921.
 PR 23-OCT-1999; 99GB-0025015.
 XX (MML-) ML LAB PLC.
 PA Lechler RI, Rogers NJ, Dorling A;
 DR WPI; 2000-442537/38.
 DR P-PDB; AAY95321.
 PT Novel methods for improving tolerance to a xenograft comprising
 PT immunizing a mammal with a T-cell epitope and a B-cell epitope -
 XX Disclosure; Fig 3; 81bp; English.
 PS The present sequence is that of cDNA clone CD86(1), which encodes
 CC pig co-stimulatory molecule CD86 (B7-2) (see AAY95321). The clone
 CC was obtained by PCR amplification of pig cDNA using primers (see
 CC AAA49662-63) based on a published pig B7-2 sequence. The invention
 CC relates to a novel strategy to inhibit costimulation by porcine
 CC cells of human T cells, with particular importance in the context
 CC of xerotransplantation of porcine organs. Recipients are immunised
 CC with hybrid synthetic peptides comprising a T cell epitope
 CC conjugated to sequences of the porcine costimulatory molecules
 CC CD80, CD86 or CD40. Peptides that induce antibodies specific for

CC regions of costimulatory molecules involved in binding to their
 CC counter-receptors on human cells (CD28 and CD14) are capable of
 CC blocking the delivery of costimulation. Once the antibody response
 CC has been induced, the transplanted organ will recall this response
 CC due to the expression of the costimulatory molecules, thereby
 CC sustaining the response, and providing an endogenous mechanism of
 CC costimulatory blockade. The method is useful for improving the
 CC tolerance of a host to xenografts, particularly porcine pancreatic
 CC islet cells.
 XX
 SQ Sequence 1050 BP; 305 A; 260 C; 227 G; 258 T; 0 other;
 Query Match 62.9%; Score 621; DB 21; Length 1050;
 Best Local Similarity 81.0%; Pred. No. 1e-176;
 Matches 804; Conservative 0; Mismatches 165; Indels 24; Gaps 6;
 Qy 10 AGATGACCTATGGAATGAAATTAACATCTCTTGTGATGACCTCTCTATGAGTGT 69
 Db 27 AGTGGATCCATGGAGCTGAGTACATCTCTTGGAGTGGCTCTCTCTCTCTGCTGT 86
 Qy 70 GCTTCATGGAAGAGTCAAGCATATTTCAACAAGCTGGAGACTGGCATTTTACA 129
 Db 87 GCCTCTTGAAGAGTCAAGCATATTTCAAGAGACTGGAGACTGGCATTTTACA 146
 Qy 130 AATTCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 189
 Db 147 AACTCGAGAACCTTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 206
 Qy 190 GTTCTGACAGCTATACAGAGCAAGAGAACCTTCAAAATTTATGCAATTAAG 249
 Db 207 GTTCTGACAGCTATACAGAGCAAGAGAACCTTCAAAATTTATGCAATTAAG 266
 Qy 250 GGCCGCAAGAGCTTGTGACAAAGCAATGTGACCTGAGACTGATTAATTCAGATCAG 309
 Db 267 GGTGCAAGAGCTTGTGACAGAGCAATGTGACCTGAGACTGATTAATTCAGATCAG 326
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 Db 327 GACAAAGGCTTGTATCAATGTTTGTTCATCAATTAAGAGGAGGAGGAGGAGGAG 386
 Qy 370 CACCAAGTGAATTCGACCTATACAGCTGATGATGATGATGATGATGATGATGATG 429
 Db 387 CACCAAGTGAATTCGACCTATACAGCTGATGATGATGATGATGATGATGATGATG 446
 Qy 430 ACTTCTAATAGAACAGAAATTTCTGGCATCAATTAATTTGACCTGATCAATTAAG 489
 Db 447 CTACTAATACACAGAAATTTCTG---TCATAAATTTGACCTGATCAATTAAG 503
 Qy 490 TACCCGAAGCCCAAGAGATGATTTTTTGTGTAACCAAGCAATTAAGTCAATTAAG 549
 Db 504 TACCCGAAGCCCAAGAGATGATTTTTTGTGTAACCAAGCAATTAAGTCAATTAAG 563
 Qy 550 GATAGTGAATGAAGAAATTCGAAATATGTCACAGCTCTACAGCTCTCTCTCTCTG 609
 Db 564 GATAGTGAATGAAGAAATTCGAAATATGTCACAGCTCTACAGCTCTCTCTCTCTG 623
 Qy 610 TTGCTCTTCAGTCCCTGAGCAAGCAATGTGACATCTTCTGTCTCTGCACTTGTAG 669
 Db 624 GTGCTCTTCAGTCCCTGAGCAAGCAATGTGACATCTTCTGTCTCTGCACTTGTAG 683
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 Db 684 CCAAGCAAGCACT 743
 Qy 721 ACCCTGATGAGAGCACATCTCTGATGATGAGGCTCTGATGATGATGATGATGATG 780
 Db 744 CCCCTGATGAGAGCACATCTCTGATGATGAGGCTCTGATGATGATGATGATGATG 803
 Qy 781 TGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 Db 804 TGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
 Qy 841 CATGAT---GTGAACCAACAAAGTGAAGAAAGAAAGTGAAGCAAGCAAGCAAGCA 897

XX Claim 1; Page 109-111; 148bp; English.
PS The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;

Query Match 71.3%; Score 704; DB 20; Length 1795;
Best Local Similarity 99.3%; Pred. No. 1.3e-201;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACATGTAAGTAATTAACATTCTCTTTGTGATGACCCCTGCTC 60
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DB TATGTCCTGCTCCATGGAAGTCAAGCATATTTCAACAAGCTGAGAACTGCGATGC 126
QY 121 CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 180
DB CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 186
QY 181 GATTAAGCTGTTCTGTACGACTATACAGAGCAAGAACCCCTCAAAATGTCATGC 240
DB GATTAAGCTGTTCTGTACGACTATACAGAGCAAGAACCCCTCAAAATGTCATGC 246
QY 241 AAGTATAAGGGCGCGACAGCTTGGACAAAGCAATTTGACCCCTGAGATCCATATAT 300
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DB CAGATCAAGACAAAGGCTTGTATCAATGTTGTCATCATTAAGGGCCCAAGAGACTC 366
QY 361 GTTCCCATGACCAAGATGTAATTCGACTATCAGTCTGTAACCTCAGTCAACCTGAA 420
DB GTTCCCATGACCAAGATGTAATTCGACTATCAGTCTGTAACCTCAGTCAACCTGAA 426
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DB TCTATAGCTTGTCTTCTTCAGTCCCTGAAGCAAGCATGTGAGCTCTTGTGTCTG 666
QY 661 CAACTTGAAGTCAAGAGCTTCCCTCCATCCTTATATATATGATGACACATA 712
DB CAACTTGAAGTCAAGAGCTTCCCTCCATCCTTATATATATGATGACACATA 718

RESULT 14
AAZ27922/c
ID AAZ27922 standard; DNA; 1795 BP.
XX
AC AAZ27922;

XX 20-DEC-1999 (first entry)
DE Canine B7-2S gene complementary DNA sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX W09947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 112-114; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
SQ Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;

Query Match 71.3%; Score 704; DB 20; Length 1795;
Best Local Similarity 99.3%; Pred. No. 1.3e-201;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACATGTAAGTAATTAACATTCTCTTTGTGATGACCCCTGCTC 60
DB ATGTATCTCAGATGACATGTAAGTAATTAACATTCTCTTTGTGATGACCCCTGCTC 66
QY 61 TATGTCCTGCTCCATGGAAGTCAAGCATATTTCAACAAGCTGAGAACTGCGATGC 120
DB TATGTCCTGCTCCATGGAAGTCAAGCATATTTCAACAAGCTGAGAACTGCGATGC 126
QY 121 CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 180
DB CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 186
QY 1669 CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 1610
DB CATTTTACAAATTCGAAAAACATAAGCTGATGAGTTGTTGGCAGAGCAG 1616
QY 181 GATAAGCTGTTCTGTACGACTATACAGAGCAAGAGAACTCTCAAAATGTTCAATGC 240
DB GATAAGCTGTTCTGTACGACTATACAGAGCAAGAGAACTCTCAAAATGTTCAATGC 246
QY 241 AAGTATAAGGGCGCGACAGCTTGGACAAAGCAATTTGAGCCCTGAGAACTGCAATAT 300
DB AAGTATAAGGGCGCGACAGCTTGGACAAAGCAATTTGAGCCCTGAGAACTGCAATAT 306
QY 301 CAGATCAAGACAAAGGCTTGTATCAATGTTCTTCATCATTAAGGCCCAAGAGACTC 360
DB CAGATCAAGACAAAGGCTTGTATCAATGTTCTTCATCATTAAGGCCCAAGAGACTC 366
QY 361 GTTCCCATGACCAAGATGTAATTCGACTATCAGTCTGTAACCTCAGTCAACCTGAA 420
DB GTTCCCATGACCAAGATGTAATTCGACTATCAGTCTGTAACCTCAGTCAACCTGAA 426

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Db 541 ACTAAGTATGATACGTGCATGGAAGAAATCTCAAAATATATGTCACAGACTCTTACAAGCTT 600
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Db 601 TCTATCAGCTTGTCTCTCAGTCCCTGAAGCAAGCAATGTAGAGACTTCTGTGTCTG 660
QY 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATATGATGACACATA 712
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Db 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATATGAAACCAACA 712

RESULT 12
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ID AA227924 standard; DNA; 840 BP.
XX
XX AA227924;
XX
XX 20-DEC-1999 (first entry)
XX
DE Complementary strand of canine B7-2S coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS.
XX
XX WPI; 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases
XX
XX Claim 1; Page 115; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
SQ Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;

Query Match 71.3%; Score 704; DB 20; Length 840;
Best Local Similarity 99.3%; Pred. No. 8.6e-202;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACATATGGAAGCAATTCCTTTGATGATGACCTCCTGCTC 60
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Db 840 ATGTATCTCAGATGACATATGGAAGCAATTCCTTTGATGATGACCTCCTGCTC 781
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QY 61 TATGGTGGCTTCATGAGAGTCAGCATATTTTCAACAAGACTGGAGACTGGCATGC 120
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QY 121 CATTTTACAATTTCTCAAAACATAGCCTGATGAGTTGTAGTTTGGCAGGACGAG 180
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Db 660 GATAAGCTGTTCTGTAGAGCTATACAGAGCAAGAAGACCTCAAAATGTTCAATGC 601
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QY 421 ATATGTAACCTCTTAATAGAACAGAAAATTCGGCATCATTAATTTGACCTGCTCATCC 480
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QY 481 ATACAGAGTTACCCAGAACCCCAAGAGATGATTTTGGTAAACCGAGAAATTCAGT 540
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Db 360 ATACAGAGTTACCCAGAACCCCAAGAGATGATTTTGGTAAACCGAGAAATTCAGT 301
    |||||||
QY 541 ACTAAGTATGATGATGTCATGAGAAGAAATCTCAAAATATATGTCACAGAACTTACAAGCTT 600
    |||||||
Db 300 ACTAAGTATGATGATGTCATGAGAAGAAATCTCAAAATATATGTCACAGAACTTACAAGCTT 241
    |||||||
QY 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCAATGTAGAGACTTCTGTGTCTG 660
    |||||||
Db 240 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCAATGTAGAGACTTCTGTGTCTG 181
    |||||||
QY 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATAGAACCAACA 712
    |||||||
Db 180 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATAGAACCAACA 129

RESULT 13
AA227921
ID AA227921 standard; DNA; 1795 BP.
XX
XX AA227921;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2S protein encoding DNA.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS.
XX
XX WPI; 1999-571822/48.
XX
XX P-PSDB; AAY41078.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases
XX
```



```

Db      319 GTACAAAGCTTTGACAAAGGACCACTGACCTGAGACTCCACAAATGTTAGATCAAGGACA 378
Oy      314 AGGCGCTTGATCAATGTTTCGTTTCATCAATAAAGGCGCCAAAGAGACTCTGCCATGACAC 373
Db      379 AGGGACATATACAGTTCATTTCATTTAAAGGCCCAAGAGACTAGTCCCATGACAC 438
Oy      374 AGATCAATTTGACATATCAGTCTGCTAACTTCAGTCAACCTGGAATTAATGGTAACCT 433
Db      439 AATAGAGTTCAGCTATCAGTCTGCTTAACCTTCAGTCAACCTGGAATTAATGTAACCT 498
Oy      434 CTATATGAGACGAAATTTCTGGCATCATAAATTTGACTGCTCATCTGCTCAAGTTCAC 493
Db      499 CTATATGAGACGAAATTTCTGGCATCATAAATTTGACTGCTCATCTGCTCAAGTTCAC 558
Oy      494 CAGAACCCAGAGAGATGATTTTGTGTAACCCGAGAAATTCAGTCAAGTTCAGTTCATA 553
Db      559 CAGAACCTAAGAGATGATTTTGTGTAACCCGAGAAATTCAGTCAAGTTCAGTTCATA 618
Oy      554 CTGTCATGAGAAATCTCAAAATTAATGTCACAGAACTTACAGCTTTCTATGAGCTTGT 613
Db      619 CTGTCATGAGAAATCTCAAAATTAATGTCACAGAACTTACAGCTTTCTATGAGCTTGT 678
Oy      614 CTTCTCAGTCCCTGACGACGACATGAGATCTTCTGCTGCTGCACTGAGTCA 673
Db      679 CTTTTCAGTCCCTGACGACGACATGAGATCTTCTGCTGCTGCACTGAGTCA 738
Oy      674 T---GAACTTCCCTCCCTACCTTATATATATATGATGACACA--TACGAAACCCACCTG 727
Db      739 TGGATATGCTGCTGCTCCCTACCTTATATATATGATGACAACTGATGATTAACCCCTG 798
Oy      728 ATGGAGACCAATCTCTGCGATTTGCGGCTCTGCTTGAATGTTGTCATTTTGTGCGGA 787
Db      799 AACCAAGGCTCTCTGCGATTTGCGGCTCTGCTTGAATGTTGTTGTTGTTGTTGTTG 858
Oy      788 TGTGTTCTTCTCTAACAATAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 847
Db      859 TGTGTTCTTCTTAAACAATAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 918
Oy      848 GTGAACCAACAAGAGTGAAGAAAGAAAGAAAGTGAAGAAAGTGAAGTGAAGTGAAGT 907
Db      919 GTGAACCAACAAGAGTGAAGAAAGAAAGAAAGTGAAGAAAGTGAAGTGAAGTGAAGT 978
Oy      908 ATGAAGCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 967
Db      979 ACGTACCTGAAGATCTGATGAAGCCAGTGTGTTAATTTGAAAGACAGCCCTCAGGGG 1038
Oy      968 ACAACAGT 975
Db      1039 ACAAAAAT 1046

```

RESULT 10
AAZ34785
ID AAZ34785 standard; cdna; 1080 BP.

XX AAZ34785;

XX 15-FEB-2000 (first entry)

XX Cat CD86 (B7-2) cDNA.

XX CD86: B7-2; ligand; cat; vaccine; feline immunodeficiency virus;

XX FIV; feline leukaemia virus; feline infectious peritonitis virus;

XX feline panleukopenia virus; feline calicivirus; feline reovirus-3;

XX feline rotavirus; feline coronavirus; feline syncytial virus;

XX feline sarcoma virus; feline herpesvirus; feline Borna disease;

XX rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;

XX parasite; autoimmune disease; transplant rejection; therapy; ss.

XX Felis domesticus.

XX Key Location/Qualifiers

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FT      CDS      63..1055
FT      /*tag= a
XX      PN      WO95/2271-A2.
XX      PD      11-NOV-1999.
XX      PE      30-APR-1999; 99MO-US09502.
XX      PR      01-MAY-1998; 98US-0071699.
XX      PA      (TEXA ) TEXAS A & M SYSTEM.
XX      PI      Collision EW, Hash SM, Choi I;
XX      DR      WPI; 2000-052972/04.
XX      PT      P-PDB; AAY32278.
XX      PT      Novel feline proteins used to produce feline vaccines which prevent
XX      PT      infectious disease or to promote growth in homologous or heterologous
XX      PT      species -
XX      PS      Claim 6; Fig 3A; 186pp; English.
XX      CC      This is the nucleotide sequence of cDNA encoding feline CD86
XX      CC      (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
XX      CC      peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
XX      CC      comprising nucleic acid encoding feline CD86 ligand or feline
XX      CC      soluble CD86 ligand is designated PSI-2/19-2/011298 (ATCC 209821).
XX      CC      The coexpression of CD86 with the costimulatory molecules CD28 (see
XX      CC      AAY32279) and a tumour antigen or an antigen from a pathogenic
XX      CC      organism has the ability to activate or enhance activation of
XX      CC      T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
XX      CC      the ability to regulate activation of T-lymphocytes. The invention
XX      CC      provides isolated nucleic acid encoding feline CD86 ligand,
XX      CC      feline CD86 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
XX      CC      (CD152) receptor, as well as vectors comprising the nucleic acids,
XX      CC      and polypeptides encoded by the nucleic acids. It also provides
XX      CC      vaccines comprising the CD86, CD86, CD28 or CTLA-4 polypeptides and
XX      CC      further comprising immunogens derived from pathogens, especially
XX      CC      feline immunodeficiency virus (FIV), feline leukaemia virus,
XX      CC      feline infectious peritonitis virus, feline panleukopenia virus,
XX      CC      feline calicivirus, feline reovirus-3, feline rotavirus, feline
XX      CC      coronavirus, feline syncytial virus, feline sarcoma virus, feline
XX      CC      herpesvirus, feline Borna disease virus, rabies virus, chlamydia,
XX      CC      Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
XX      CC      pathogen, or parasite (all claimed). Vaccines capable of
XX      CC      enhancing an immune response, and vaccines capable of suppressing
XX      CC      an immune response (suitable for treating an autoimmune disease
XX      CC      or tissue or organ transplant rejection) are claimed. The
XX      CC      nucleic acids may be used for gene therapy or antisense therapy
XX      CC      protocols.
XX      SQ      Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

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Query Match 78.3%; Score 772.8; DB 21; Length 1080;

Best Local Similarity 88.8%; Pred. No. 1.8e-22;

Matches 860; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

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Oy      14 GCACATGGAAGTGAATATCATTTCTTTGATGATGACCTCTGCTCATAGTGTGCTT 73
Db      79 GCATATGGAAGTGAATATCATTTCTTTGATGATGATGATGATGATGATGATGAT 138
Oy      74 CCATGAGAGTCAAGCATTTTCAACAAGAGAGAGAGTGCATGCAATTTTACAAAT 133
Db      139 CCATGAGAGTCAAGCATTTTCAACAAGAGAGAGTGCATGCAATTTTACAAAT 198
Oy      134 CTCAAAACATTAAGCTGTAGTGTGTTGTTGTCAGAGCAGAGATAGCTGTTC 193
Db      199 CTCAAAACATTAAGCTGTAGTGTGTTGTTGTCAGAGCAGAGATAGCTGTTC 258
Oy      194 TGTAGAGCTATACAGAGGCAAGAAAGAAAGTCAAAATGTTTCATGCAAGTAAAGGCGC 253

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Db 2576 CCATGAAAGCAAGCAATATTTCAACAAGACTGGAGAACTGCCATTATTTCAAACT 2517
Oy 134 CTCAAAACATAGAGCTGGATGAGTGTGATGTTTGGCAGACAGAGATTAAGCTGTTC 193
Db 2516 CTCAAAACATAGAGCTGGATGAGTGTGATGTTTGGCAGACAGAGATTAAGCTGTTC 2457
Oy 194 TGTACGACTATACAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 253
Db 2456 TGTATAGATATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAAATATAGGGCC 2397
Oy 254 GCACAGAGCTTTGACAAACAAATGGACCCGAGACCTCATTAATATGATCAAGACACA 313
Db 2396 GTACAGAGCTTTGACAAAGCAACTGGACCTGAGACTCCACAAATGTTTCAGATCAAGGACA 2337
Oy 314 AGGCTGTATCATATGTTTGTCTCATTAAGAGGCCCAAGAGACTGCTCCATGCACC 373
Db 2336 AGGCAACATATCACTGTTTCATTTATTAAGGCCCAAGAGACTAGTCCCATGCACC 2277
Oy 374 AGATGAATTCGACCTATACAGTGTGCTGTAACCTCAGTCAACCTGAATATGTAACCT 433
Db 2276 AATAGAGTTCGACCTATACAGTGTGCTGTAACCTCAGTCAACCTGAATATGTAACCT 2217
Oy 434 CTAATAGAACAGAAATCTGSCATCATAAATTTGACCTGCTCATCATACAGAGTTACC 493
Db 2216 CTAATAGAACAGAAATCTGSCATCATAAATTTGACCTGCTCATCATACAGAGTTACC 2157
Oy 494 CAGAACCCAGAGAGATGATTTTTTGTGTAACCCAGAAATTCAGTCAATGATGATA 553
Db 2156 CAGAACCTTAGAGAGATGATTTTTTGTGTAACCCAGAAATTCAGTCAATGATGATA 2097
Oy 554 CAGTATAGAGAAATCTCAAAATATGTCAGAACTGTACAAAGCTTCTATCAGCTTGT 613
Db 2096 CAGTATAGAGAAATCTCAAAATATGTCAGAACTGTACAAAGCTTCTATCAGCTTGT 2037
Oy 614 CCTTCAGTCCCTGAGCAAGCAATGTGACATCTTGTGTCTGCACTTGAATGCA 673
Db 2036 CTTTTCAGTCCCTGAGCAACATGTGAGCGTCTTTGTGCTGCAACTGAGAGAC 1977
Oy 674 T---GAAGTTCCTCCCTACCTTATATATGATGACACA---TACGAACCCAGCCCTG 727
Db 1976 TGGAGATGCTGCTCCCTACCTTCAATATGATGACACAACTAAGGATTAAGACCTG 1917
Oy 728 ATGAGAACACATCTCTGATTTGGCGCTCTGCTGTATGTTGGTCAATTTTGTGGGA 787
Db 1916 AACAGAGCACTCTCTGATTTGGCGCTCTGCTGTATGTTTGTGTTTGTGGGA 1857
Oy 788 TGGTGTCTTCTTACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 1856 TGGTGTCTTCTTAAACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797
Oy 848 GTGAAGCAACAAAGTGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Db 1796 GTGAAGCAACAAAGTGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
Oy 908 ATGAAGAGAGAAAGATGATGAGAGCCAGTGTGTTAACTTTGAAGAGAGAGAGAGAG 967
Db 1736 AGTACCTGAGAGATGATGAGAGCCAGTGTATTAACATTTTGAAGAGAGAGAGAG 1677
Oy 968 ACAACAGTACTACAGAGTTT 987
Db 1676 ACAAAAGTACTACACATTTT 1657

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XX
KW CD86; B7-2; feline; cat; recombinant virus; vaccine;
KW Immunomodulator; tumour; cancer; therapy; ss.
XX
OS Fells domesticus.
XX
FH Key Location/Qualifiers
FT CDS 63..1052
FT /tag=a
XX
PN WO957295-A1.
XX
PD 11-NOV-1999.
XX
PE 30-APR-1999; 99WO-US09504.
XX
PR 01-MAY-1998; 98US-0071711.
XX
PA (SCHE ) SCHERING-PLOUGH LTD.
PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX
PI Winslow BJ, Cochran MD;
XX
DR MPI; 2000-062155/05.
XX
DR P-SDB; AAY32285.
XX
PT Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines
XX
PS Disclosure; Fig 3a; 230pp; English.
XX
CC This is the nucleotide sequence of cDNA coding for feline CD86
CC (B7-2). The cDNA was isolated from feline peripheral blood
CC mononuclear cell cDNA by PCR. Manipulating the expression of CD28
CC or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC regulates T cell proliferation and cytokine release. The invention
CC relates to a recombinant virus that contains at least one foreign
CC nucleic acid, inserted into a nonessential genomic region, that
CC encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
CC immunogenic fragments, and is expressed when the recombinant virus
CC is introduced into a suitable host. The invention also provides:
CC a recombinant virus further comprising a foreign nucleic acid
CC encoding an immunogen derived from a feline pathogen; recombinant
CC viruses capable of enhancing an immune response to protect against
CC disease; recombinant viruses expressing antisense sequences,
CC capable of suppressing an immune response in a feline, e.g., for
CC treatment of autoimmune disease or transplant rejection; and
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used
CC to reduce or eliminate a tumour in cats.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

Query Match 78.3%; Score 772.8; DB 21; Length 1080;
Best Local Similarity 88.8%; Pred. No. 1.8e-222;
Matches 860; Conservative 0; Mismatches 102; Indels 6; Gaps 2;
Oy 14 GCATATGAGAACTGAATATCTCTTGTGATGACCTCTGCTTATGCTGCTT 73
Db 79 GCATATGAGAACTGAATATCTCTTGTGATGAGGCTCTCTCTCTGCTGCTT 138
Oy 74 CCATGAAGAGTCAAGCATATTTCAACAAAGACTGGAGAGAGAGAGAGAGAGAGAG 133
Db 139 CCATGAAGAGTCAAGCATATTTCAACAAAGACTGGAGAGAGAGAGAGAGAGAGAG 198
Oy 134 CTCAAAACATAGAGCTGGATGAGTGTGATGTTTGGCAGACAGAGATTAAGCTGTTC 193
Db 199 CTCAAAACATAGAGCTGGATGAGTGTGATGTTTGGCAGACAGAGATTAAGCTGTTC 258
Oy 194 TGTACGACTATACAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 253
Db 259 TGTATAGATATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAAATATAGGGCC 318
Oy 254 GCACAGAGCTTTGACAAACAAATGGACCTGAGACTCCATTAATATGATCAAGACACA 313

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PT treating, e.g. autoimmune and atopic diseases -
 XX
 PS Claim 1; Page 116-119; 148bp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 2830;
 Best Local Similarity 89.0%; Pred. No. 7e-226;
 Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGGAAGTGAATACATCTCTTTGATGAGACCCCTGCTATAGTGTGCTT 73
 DB 195 GCATGTGGAGTGAAGTGAATACATCTCTTTGATGAGACCCCTGCTATAGTGTGCTT 254
 QY 74 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATTTTACAAT 133
 DB 255 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATTTTACAAT 314
 QY 134 CTCAAAACATAGCTGTGATGATGTTGTTGGCAGAGACAGATTAAGCTGTT 193
 DB 315 CTCAAAACATAGCTGTGATGATGTTGTTGGCAGAGACAGATTAAGCTGTT 374
 QY 194 TGTAGAGCTATACAGGAGCAAGAAACCTCAAAATGTTTCAATCGCAATTAAGGCC 253
 DB 375 TGTATGATATATTCAGAGCAAGAAACCTCAAAATGTTTCAATCGCAATTAAGGCC 434
 QY 254 GCACAAGCTTTGACAAAGACATTTGGACCTGACATTCATATTTCAATCAAGACA 313
 DB 435 GTACAAAGCTTTGACAAAGACATTTGGACCTGACATTCATATTTCAATCAAGACA 494
 QY 314 AGGGCTTATCAATGTTCTGTCATCATTAAGGGCCCAAGAGCTGTTCCATGAC 373
 DB 495 AGGGCAATATTCATGTTCTGTCATCATTAAGGGCCCAAGAGCTGTTCCATGAC 554
 QY 374 AGATGAATTTGACCTATCACTGCTTGTGCTAACTGACCTGAATTAAGTAT 433
 DB 555 AATGATGTTGACCTATCACTGCTTGTGCTAACTGACCTGAATTAAGTAT 614
 QY 434 CTAAATGAAGCAAAATTTCTGACATCAATTTTGAACCTGCTCATATACAGTTACC 493
 DB 615 CTAAATGAAGCAAAATTTCTGACATCAATTTTGAACCTGCTCATATACAGTTACC 674
 QY 494 CAGAACCCAGAGATGATTTTTTGTAAACCCAGCAATTTCAAGTACTAAGTAT 553
 DB 675 CAGAACCCAGAGATGATTTTTTGTAAACCCAGCAATTTCAAGTACTAAGTAT 724
 QY 554 CCGTATGAAGAACTCAAAATATGACAGAACTCAAGCTTCAATCAAGCTTGT 613
 DB 735 CCGTATGAAGAACTCAAAATATGACAGAACTCAAGCTTCAATCAAGCTTGT 794
 QY 614 CCGTATGAAGAACTCAAAATATGACAGAACTCAAGCTTCAATCAAGCTTGT 673
 DB 795 CCGTATGAAGAACTCAAAATATGACAGAACTCAAGCTTCAATCAAGCTTGT 854
 QY 674 T---GAAGCTTCCCTGCTATATATATATATGACACA---TAGCAACCCACCTG 727
 DB 855 TGAAGTGTGCTGCTCCCTGCTATATATATATATGACACA---TAGCAACCCACCTG 914
 QY 728 ATGAAGACACATCTGATGATGAGGCTGCTGATGATGATGATGATGATGATG 787
 DB 915 AACAGGACACTCTCTGATGAGGCTGCTGATGATGATGATGATGATGATG 974
 QY 788 TGGTGTCTTTCTAAGCACTAAGAAAGAAAGAAAGCAAGCAAGCTGAGCCCTCTCATGAT 847

DB 975 TGGTGTCTTTAAGCACTAAGAAAGAAAGAAAGCAAGCAAGCTGAGCCCTCTCATGAT 1034
 QY 848 GTGAACCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
 DB 1035 GTGAACCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1094
 QY 908 ATGAAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 967
 DB 1095 ACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1154
 QY 968 ACAACAGTACTACACAGTTT 987
 DB 1155 ACAACAGTACTACACATTTT 1174

RESULT 8
 AA227930/C
 ID AA227930 standard; DNA; 2830 BP.
 XX
 NC AA227930;
 DT 20-DEC-1999 (first entry)
 XX
 DE Feline B7-2 gene complementary DNA sequence.
 XX
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; feline;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 XX
 OS Fells catus.
 XX
 PN W09947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06187.
 XX
 PR 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Sellins KS;
 DR WPI; 1999-571822/48.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 XX
 PS Claim 1; Page 121-123; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 2830;
 Best Local Similarity 89.0%; Pred. No. 7e-226;
 Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGGAAGTGAATACATCTCTTTGATGAGACCCCTGCTATAGTGTGCTT 73
 DB 255 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATTTTACAAT 314
 QY 74 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATTTTACAAT 133

DE Complementary strand of feline B7-2 coding sequence.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
OS
PN WO947558-A2.
XX
XX 23-SEP-1999.
PD
XX 19-MAR-1999; 99WO-US06187.
PF
XX 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
PA
PI Sim G, Yang S, Sellins KS;
PI
XX WPI; 1999-571822/48.
DR
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
XX
PS Claim 1; Page 124-125; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
CC
XX
SQ Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 996;
Best Local Similarity 89.0%; Pred. No. 4.1e-226;
Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGAGAACTGAATTAACATCTCTTGTGATGACCCCTGCTCTATGAGTGTCTT 73
DB 980 GCACATGAGAACTGAATTAACATCTCTTGTGATGACCCCTGCTCTATGAGTGTCTT 921
QY 74 CCATGAAGAGCTCAAGCATATTTCAACAGAGCTGAGAACTGCGATGCCATTTTACAAT 133
DB 920 CCATGAAGAGCTCAAGCATATTTCAACAGAGCTGAGAACTGCGATGCCATTTTACAAT 861
QY 134 CTGAAACATTAAGCGTGGATGAGTGTGTGATGTTGGCGAGGACGAGATTAACGTGTT 193
DB 860 CTGAAACATTAAGCGTGGATGAGTGTGTGATGTTGGCGAGGACGAGATTAACGTGTT 801
QY 194 TGTACGAGCTATACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 253
DB 800 TGTATGAGATATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 741
QY 254 GCACAGCTTTGACAAAG 313
DB 740 GTAAACCTTTGACAAAG 681
QY 314 AGGCTGTATCATGTTTGGTTCATCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 373
DB 680 AGGCTGTATCATGTTTGGTTCATCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621
QY 374 AGATGAATTTGACATTAAG 433
DB 620 AATGAGTCTGACATTAAG 561
QY 434 CTATTAAG 493

DB 560 CTAATGAG 501
QY 494 CAGAACCCAG 553
DB 500 CAGAACCTTAAG 441
QY 554 CTGTATGAG 613
DB 440 CTGTATGAG 381
QY 614 CCTTCTGAGTCCCTGAG 673
DB 380 CTTTTCAGTCCCTGAG 321
QY 674 T---GAAGCTTCCCTGAG 727
DB 320 TGGAGATGCTGCTCTCTCCCTACCTTTCAATATATGATGACAACTTAAGATTAAGAGAGAG 261
QY 728 ATGAGAGCCAGATCCTGAGATGAG 787
DB 260 AACAAGGCCAGATCCTGAGATGAG 201
QY 788 TGGTCTTTCTTAACATTAAG 847
DB 200 TGGTCTTTCTTAACATTAAG 141
QY 848 GTGAAGCCAG 907
DB 140 GTGAAGCCAG 81
QY 908 ATGAAGCCAG 967
DB 80 ACGTACCTGAG 21
QY 968 ACAAGAGTACTACAGAGTTT 987
DB 20 ACAGAAAGTACTACAGATTTT 1

RESULT 7
AAZ27929
ID AAZ27929 standard; DNA; 2830 BP.
XX
XX AAZ27929;
XX
XX 20-DEC-1999 (first entry)
XX
DE Feline B7-2 protein encoding DNA.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
OS
XX
XX WO947558-A2.
PN
XX
XX 23-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-US06187.
PF
XX 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX
XX (HESK-) HESKA CORP.
PA
PI Sim G, Yang S, Sellins KS;
PI
XX WPI; 1999-571822/48.
DR P-PSDB; AAY41079.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

Db 1112 TGTGGATGTCTTCTTCTTACACTAAGGAAAGAAAGAACAGCAGCCGCCCCCT 1053
QY 841 CATTGATGTGAACCAACAAAGTGTGAGAGAAAGAAAGTGTGACAGACCAAGAGAGTA 900
Db 1052 CATTGATGTGAACCAACAAAGTGTGAGAGAAAGAAAGTGTGACAGACCAAGAGAGTA 993
QY 901 CGGTACCATGAAGCGAAAGATCTGATGAGCCAGTGTGTTAACATTTCGAAGCAGCT 960
Db 992 CGGTACCATGAAGCGAAAGATCTGATGAGCCAGTGTGTTAACATTTCGAAGCAGCT 933
QY 961 TCAGCGCAGACAGTACTACACAGTTT 987
Db 932 TCAGCGCAGACAGTACTACACAGTTT 906

RESULT 5

AAZ27931
ID AAZ27931 standard; DNA; 996 BP.

AC AAZ27931;

DT 20-DEC-1999 (first entry)

DE Feline B7-2 protein coding sequence.

XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

KM allergic reaction; infectious disease; tumor development; feline;

KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Felis catus.

FN W09947558-A2.

XX 23-SEP-1999.

PD 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

PI Slim G, Yang S, Sellins KS;

XX WPI: 1999-571822/48.

DR P-PSDB: AAY41079.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

PT treating, e.g. autoimmune and atopic diseases

XX Claim 1; Page 123-124; 148pp; English.

PS The invention provides B7 and CTLA4 (T cell costimulatory proteins)

XX CC encoding nucleic acid molecules from dogs and cats. The proteins can be

CC expressed by standard recombinant methodology. The nucleic acid molecules

CC and the encoded proteins can be used for preventing or treating diseases,

CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

CC development, graft rejection, inflammation, arthritis and atopic diseases

CC such as atopic dermatitis. They can be used in mammals such humans, dogs,

CC cats, cattle, sheep or pets. The products can also be used for detection,

XX diagnosis and drug screening.

XX Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 996;

Best Local Similarity 89.0%; Pred. No. 4,1e-226;

Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGAGACGATGATATCTCTTTGTGATGAGCCCTGCTCTATGATGCTGCTT 73
Db 17 GCACATGAGACGATGATGATATCTCTTTGTGATGAGCCCTGCTCTATGATGCTGCTT 76

QY 74 CCATGAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGCTATTTACAATT 133
Db 77 CCATGAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGCTATTTACAAACT 136
QY 134 CTCAAAACATTAAGCCTGGATGAGTGTGATGTTTGGCAGGACCAAGATTAAGCTGTTG 193
Db 137 CTCAAAACATTAAGCCTGGATGAGTGTGATGTTTGGCAGGACCAAGATTAAGCTGTTG 196
QY 194 TGTGAGCTATATACAGAGCAAGAACCTCAAAATGTTTCATCGCAATATTAAGGCC 253
Db 197 TGTATGAGATATTCAGAGCAAGAACCTCAAAATGTTTCATCGCAATATTAAGGCC 256
QY 254 GCACACCTTTGACAAAGACAATTTGGACCTGAGACCTCAATATTCATCAATCAAGACA 313
Db 257 GTACAGCTTTGACAAAGACAATTTGGACCTGAGACCTCAATATTCATCAATCAAGACA 316
QY 314 AGGCTTGTATCAATGTTTGTTCATCATTAAGAGCCCAAGAGACTGTTCCATGACC 373
Db 317 AGGCAATATCACTGTTTATTCATCATTAAGAGCCCAAGAGACTGTTCCATGACC 376
QY 374 AGATGAATTCGACCTATCACTGCTTGTCTACTTCACTCACTGAATTAATGTAATT 433
Db 377 AAATGAGTTCTGACCTATCACTGCTTGTCTACTTCACTCACTGAATTAATGTAATT 436
QY 434 CTATATGACAGAAATTTTGGCATCATTAATTTGACCTGCTCATCATCAAGGTTACC 493
Db 437 CTATATGACAGAAATTTTGGCATCATTAATTTGACCTGCTCATCATCAAGGTTACC 496
QY 494 CAGAACCAAGAGATGATATTTTGTGTAACCAAGCAATTCAGTAACTAATGATGATA 553
Db 497 CAGAACCAAGAGATGATATTTTGTGTAACCAAGCAATTCAGTAACTAATGATGATA 556
QY 554 CTGTCATGAAGAAATCTCAAAATATATGTCAGAACTCAACCTTCTATCACTGTTGT 613
Db 557 CTGTCATGAAGAAATCTCAAAATATATGTCAGAACTCAACCTTCTATCACTGTTGT 616
QY 614 CTTTTCAGTCCCTGGAAGCAAGCAATGTGAGCATCTTGTGTCGCAACTGTAAGTCAA 673
Db 617 CTTTTCAGTCCCTGGAAGCAAGCAATGTGAGCATCTTGTGTCGCAACTGTAAGTCAA 676
QY 674 T---GAAGCTTCCCTGCTCACTTATTAATTAATGATGACA---TACGAACCCAGCCCTG 727
Db 677 TGAAGATGCTGCTCCCTGCTCACTTATTAATTAATGATGACA---TACGAACCCAGCCCTG 736
QY 728 ATGAGACCAACATCTCTGATGATGCGCTGCTGTGTAATGTTGTCATTTGTGAGGA 787
Db 737 AACAAGCCACTTCTCTGATGATGCGCTGCTGTGTAATGTTGTCATTTGTGAGGA 796
QY 788 TGTGTTCTTTTCAACATTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 797 TGTGTTCTTTTCAACATTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
QY 848 GTGAACCAACAAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Db 857 GTGAACCAACAAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
QY 908 ATGAAGCGAAAGATGTGATGAAGCCCACTGTTGTTAACATTTGCAAGAGAGAGAG 967
Db 917 ACCTACTAGAGATGTGATGAAGCCCACTGTTGTTAACATTTGCAAGAGAGAGAG 976
QY 968 ACAACAGTACTACACAGTTT 987
Db 977 ACAAAAGTACTACACATTTT 996

RESULT 6

AAZ27932/c

ID AAZ27932 standard; DNA; 996 BP.

AC AAZ27932;

DT 20-DEC-1999 (first entry)

```
OY 421 ATAAATGTAAGTCTTAATATGACAGAAAAATTCGTGCATCATTAATTTGACCTGCTCATCC 480
    |||||||
DB 426 ATAAATGTAAGTCTTAATATGACAGAAAAATTCGTGCATCATTAATTTGACCTGCTCATCC 485
OY 481 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGTAAAAACCGAGAAATTCAGAT 540
    |||||||
DB 486 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGTAAAAACCGAGAAATTCAGAT 545
OY 541 ACTAAGTATGATCTGTATGTAAGAAATTCATAAATATATGTCACAGAACTCTACAACTT 600
    |||||||
DB 546 ACTAAGTATGATCTGTATGTAAGAAATTCATAAATATATGTCACAGAACTCTACAACTT 605
OY 601 TCTATCAGCTTGTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCCTG 660
    |||||||
DB 606 TCTATCAGCTTGTCTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCCTG 665
OY 661 CAACCTGATGATGAGAGCTTCCCTCCCTCACTTATATATGATGACATATGCAAAACC 720
    |||||||
DB 666 CAACCTGATGATGAGAGCTTCCCTCCCTCACTTATATATGATGACATATGCAAAACC 725
OY 721 ACCCGTGAATGAGAGACCATCTCTGATGAGGCTGCTGATGATGTTGGTCAATTTTG 780
    |||||||
DB 726 ACCCGTGAATGAGAGACCATCTCTGATGAGGCTGCTGATGATGTTGGTCAATTTTG 785
OY 781 TGTGGGATGCTGTTCTTTCTTAACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 840
    |||||||
DB 786 TGTGGGATGCTGTTCTTTCTTAACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 845
OY 841 CATGATATGTAAGCAACAAAGTGGAGAGAAAGAAAGTGAACCAACCAAGAGAGAGAGAG 900
    |||||||
DB 846 CATGATATGTAAGCAACAAAGTGGAGAGAAAGAAAGTGAACCAACCAAGAGAGAGAGAG 905
OY 901 CGGTACCATGAAACCGAAGATCTGATGAAGCCAGTGTGTTAAGATTTGCAAGACAGT 960
    |||||||
DB 906 CGGTACCATGAAACCGAAGATCTGATGAAGCCAGTGTGTTAAGATTTGCAAGACAGT 965
OY 961 TCAGGCGACACAGTACTACACAGTTT 987
    |||||||
DB 966 TCAGGCGACACAGTACTACACAGTTT 992
    |||||||

RESULT 4
AAZ27914/c
ID AAZ27914 standard; DNA; 1897 BP.
XX
XX AAZ27914;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2 gene complementary DNA sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX WO94/7558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
```

```
PT treating, e.g. autoimmune and atopic diseases
XX
XX Claim 1; Page 101-102; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;
XX
XX Query Match 100.0%; Score 987; DB 20; Length 1897;
XX Best Local Similarly 100.0%; Pred. No. 6.4e-287;
XX Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTATCTCAGATGCTACTATGAGAACTGAATTAACATTCCTCTTGTGATGACCTCTGCTC 60
    |||||||
DB 1892 ATGTATCTCAGATGCTACTATGAGAACTGAATTAACATTCCTCTTGTGATGACCTCTGCTC 1833
OY 61 TATGTCGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
    |||||||
DB 1832 TATGTCGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 1773
OY 121 CATTTTCAAAATTCGAAACCATTAAGCCTGGATGAGTGGAGTGTGGAGAGACAG 180
    |||||||
DB 1772 CATTTTCAAAATTCGAAACCATTAAGCCTGGATGAGTGGAGTGTGGAGAGACAG 1713
OY 181 GATAGAGCTGTTCTGTACGAGCTATACAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
    |||||||
DB 1712 GATAGAGCTGTTCTGTACGAGCTATACAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1653
OY 241 AAGTATTAAGGGCCGACACAGCTTTGACAAAGACATTTGAGACCTGAGACTCCATTAAT 300
    |||||||
DB 1652 AAGTATTAAGGGCCGACACAGCTTTGACAAAGACATTTGAGACCTGAGACTCCATTAAT 1593
OY 301 CAGATCAAGAGAGAGGGGTTGATCAATGTTCTGTCATCAATAAGGCCCAAGGACTC 360
    |||||||
DB 1592 CAGATCAAGAGAGAGGGGTTGATCAATGTTCTGTCATCAATAAGGCCCAAGGACTC 1533
OY 361 GTTCCATGACACAGATGAATTTGACCTATACAGTGTGCTTGTACCTCACTCAACCTGAA 420
    |||||||
DB 1532 GTTCCATGACACAGATGAATTTGACCTATACAGTGTGCTTGTACCTCACTCAACCTGAA 1473
OY 421 ATATGTAACCTTCTATATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCC 480
    |||||||
DB 1472 ATATGTAACCTTCTATATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCC 1413
OY 481 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGTAAAAACCGAGAAATTCAGAT 540
    |||||||
DB 1412 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGTAAAAACCGAGAAATTCAGAT 1553
OY 541 ACTAAGTATGATCTGTATGTAAGAAATTCATAAATATATGTCACAGAACTCTACAACTT 600
    |||||||
DB 1352 ACTAAGTATGATCTGTATGTAAGAAATTCATAAATATATGTCACAGAACTCTACAACTT 1293
OY 601 TCTATCAGCTTGTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCCTG 660
    |||||||
DB 1292 TCTATCAGCTTGTCTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCCTG 1233
OY 661 CAACCTGATGATGAGAGCTTCCCTCCCTCACTTATATATAGATGACATATGCAAAACC 720
    |||||||
DB 1232 CAACCTGATGATGAGAGCTTCCCTCCCTCACTTATATATAGATGACATATGCAAAACC 1173
OY 721 ACCCGTGAATGAGAGACCATCTCTGATGAGGCTGCTGTTGAATGTTGGTCAATTTTG 780
    |||||||
DB 1172 ACCCGTGAATGAGAGACCATCTCTGATGAGGCTGCTGTTGAATGTTGGTCAATTTTG 1113
OY 781 TGTGGGATGCTGTTCTTTCTTAACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
    |||||||
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OY 61 TATGTCGTCGTCCTCCATGAGAGTCATATTTTCACAGACTGAGAGACTGCCATGC 120
DB 927 TATGGTGCTGCTTCATGAGAGTCATATTTTCACAGAGACTGAGAGACTGCCATGC 868
OY 121 CATTTTACAATTTCTCAAAACATTAAGCCCGATGAGTTGTTGTTTGGAGAGACCAG 180
DB 867 CATTTTACAATTTCTCAAAACATTAAGCCCGATGAGTTGTTGTTTGGAGAGACCAG 808
OY 181 GATTAAGCTGGTTCTGTACAGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 240
DB 807 GATTAAGCTGGTTCTGTACAGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 748
OY 241 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAATTTGACCTGACATCAATATTT 300
DB 747 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAATTTGACCTGACATCAATATTT 688
OY 301 CAGATCAAGAGCAAGGGCTTGTATCAATGTTCTGTCATCAATTAAGGGCCCAAGAGACTC 360
DB 687 CAGATCAAGAGCAAGGGCTTGTATCAATGTTCTGTCATCAATTAAGGGCCCAAGAGACTC 628
OY 361 GTTCCCATGCAACAGATGATGATTCGACCTATACAGTGTGCTGTAAGTCAAGTCAAGTCAA 420
DB 627 GTTCCCATGCAACAGATGATGATTCGACCTATACAGTGTGCTGTAAGTCAAGTCAAGTCAA 568
OY 421 ATTAATGCTACTTCTTAATBGAACAGAAAATTTGCGCATCAATTAATTTGACCTGCTCATCC 480
DB 567 ATTAATGCTACTTCTTAATBGAACAGAAAATTTGCGCATCAATTAATTTGACCTGCTCATCC 508
OY 481 ATACAAGGTTACCCAGAAACCCCAAGAGATGATTTTGGTAAACCCGACAATTTCAAGT 540
DB 507 ATACAAGGTTACCCAGAAACCCCAAGAGATGATTTTGGTAAACCCGACAATTTCAAGT 448
OY 541 ACTAAGTATGATACTGTCATGAGAAATCTCAAAATTAATGTCACAGAACTGTACAACTGT 600
DB 447 ACTAAGTATGATACTGTCATGAGAAATCTCAAAATTAATGTCACAGAACTGTACAACTGT 388
OY 601 TCTATCAGCTTGTCTTCTCAAGTCCCTCAAGCAGCAATGAGCATCTTGTGTCCTG 660
DB 387 TCTATCAGCTTGTCTTCTCAAGTCCCTCAAGCAGCAATGAGCATCTTGTGTCCTG 328
OY 661 CAACCTTGATGATGAGACTTCCCTCCCTACCTTATATATAGATGACATACGAAACCC 720
DB 327 CAACCTTGATGATGAGACTTCCCTCCCTACCTTATATATAGATGACATACGAAACCC 268
OY 721 ACCCTGATGAGAGACACATCCTCTGATGCGGCTCTGCTTGTATGTTGTTGTCATTTTG 780
DB 267 ACCCTGATGAGAGACACATCCTCTGATGCGGCTCTGCTTGTATGTTGTTGTCATTTTG 208
OY 781 TGTGGGATGGTGTCTTCTTAACACTAGGAAAGAAAGAAAGAAAGCAAGCCCTGCCCTCT 840
DB 207 TGTGGGATGGTGTCTTCTTAACACTAGGAAAGAAAGAAAGAAAGCAAGCCCTGCCCTCT 148
OY 841 CATGAATGTGAACCAACAAAGTGGAGAAAGAAAGAAAGTGGAGACCAAGAGAAAGATTA 900
DB 147 CATGAATGTGAACCAACAAAGTGGAGAAAGAAAGAAAGTGGAGACCAAGAGAAAGATTA 88
OY 901 CGGTATCACTGAAGAGGAAAGATCTGATGAGAGCCCAAGTGTGTTAAATTTGGAAGACAGCT 960
DB 87 CGGTATCACTGAAGAGGAAAGATCTGATGAGAGCCCAAGTGTGTTAAATTTGGAAGACAGCT 28
OY 961 TCAGGCGCAACAGTACTACAGAGTTT 987
DB 27 TCAGGCGCAACAGTACTACAGAGTTT 1
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RESULT 3
AA227913
ID AA227913 standard; DNA; 1897 BP.
XX
AC AA227913:
XX
DT 20-DEC-1999 (first entry)
XX

```
DE Canine B7-2 protein encoding DNA.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN W09947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
DR P-PSDB; AAT41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 97-99; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other:
Query Match 100.0%; Score 987; DB 20; Length 1897;
Best Local Similarity 100.0%; Pred. No. 6.4e-287;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGATCTCGATGACGACTATGAGAGTGAATTAATTAATTTCTTTGATGACCCCTCGCTC 60
DB 6 ATGATCTCGATGACGACTATGAGAGTGAATTAATTAATTTCTTTGATGACCCCTCGCTC 65
OY 61 TATGTCGTCGTCCTCCATGAGAGTCATATTTTCACAGACTGAGAGACTGCCATGC 120
DB 66 TATGTCGTCGTCCTCCATGAGAGTCATATTTTCACAGAGACTGAGAGACTGCCATGC 125
OY 121 CATTTTACAATTTCTCAAAACATTAAGCCCGATGAGTTGTTTGGAGAGACCAG 180
DB 126 CATTTTACAATTTCTCAAAACATTAAGCCCGATGAGTTGTTTGGAGAGACCAG 185
OY 181 GATTAAGCTGGTTCTGTACAGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 240
DB 186 GATTAAGCTGGTTCTGTACAGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 245
OY 241 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAATTTGACCTGAGACTCATATATTT 300
DB 246 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAATTTGACCTGAGACTCATATATTT 305
OY 301 CAGATCAAGAGCAAGGGCTTGTATCAATGTTCTGTCATCAATTAAGGGCCCAAGAGACTC 360
DB 306 CAGATCAAGAGCAAGGGCTTGTATCAATGTTCTGTCATCAATTAAGGGCCCAAGAGACTC 365
OY 361 GTTCCCATGCAACAGATGATGATTCGACCTATACAGTGTGCTGTAAGTCAAGTCAAGTCAA 420
DB 366 GTTCCCATGCAACAGATGATGATTCGACCTATACAGTGTGCTGTAAGTCAAGTCAAGTCAA 425
```

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 102-103; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ

Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 100.0%; Score 987; DB 20; Length 987;
Best Local Similarity 100.0%; Pred. No. 4.6e-287;

Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTATCTCAGATGACACTATGGAACATTAACATTCTCTTTGTGATGACCCCTCGCTC 60
DB 1 ATGTATCTCAGATGACACTATGGAACATTAACATTCTCTTTGTGATGACCCCTCGCTC 60
QY 61 TATGCTGCTGCTTCATGGAAGATCAAGATATTTCAACAGACTGAGAACCTGCATGC 120
DB 61 TATGCTGCTGCTTCATGGAAGATCAAGATATTTCAACAGACTGAGAACCTGCATGC 120
QY 121 CATTTTACAAATTCCTCAAAACATTAAGCTTGATGACTTGTGTGTTGGCAGACAG 180
DB 121 CATTTTACAAATTCCTCAAAACATTAAGCTTGATGACTTGTGTGTTGGCAGACAG 180
QY 181 GATTAAGCTGTTCTGTACAGAGCTATACAGAGCAAGCAACCCCTCAAAATGTTCAATGC 240
DB 181 GATTAAGCTGTTCTGTACAGAGCTATACAGAGCAAGCAACCCCTCAAAATGTTCAATGC 240
QY 241 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAAATTTGACCCCTGACCTCAATATAT 300
DB 241 AAGTATTAAGGGCCGCAACAGCTTTGACAAAGACAAATTTGACCCCTGACCTCAATATAT 300
QY 301 CGATCAAGAGCAAGGGCTTGATCAATGTTTCGTTCAATCAATTAAGGGCCCAAGACATC 360
DB 301 CGATCAAGAGCAAGGGCTTGATCAATGTTTCGTTCAATCAATTAAGGGCCCAAGACATC 360
QY 361 GTTCCCATGCACCAAGATGATTCGACCTATCATAGTCTTGTCAATCTCACTCAACTGAA 420
DB 361 GTTCCCATGCACCAAGATGATTCGACCTATCATAGTCTTGTCAATCTCACTCAACTGAA 420
QY 421 ATTAATGTAAGTCTTAATTAAGAAAGAAATTTCTGSCATATAAATTTGACCTGCTCATCC 480
DB 421 ATTAATGTAAGTCTTAATTAAGAAAGAAATTTCTGSCATATAAATTTGACCTGCTCATCC 480
QY 481 ATTAACAAGTTACCCGCAACCAAGAGATGATATTTTGGTAAAAACCGAGATTTCAAGT 540
DB 481 ATTAACAAGTTACCCGCAACCAAGAGATGATATTTTGGTAAAAACCGAGATTTCAAGT 540
QY 541 ACTAAGTATGATAGTCTGATGAAGAAATCTCAAAATATATGTCACAGACTCTCAACGTT 600
DB 541 ACTAAGTATGATAGTCTGATGAAGAAATCTCAAAATATATGTCACAGACTCTCAACGTT 600
QY 601 TCTATCAGCTTGTCTTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGCTG 660
DB 601 TCTATCAGCTTGTCTTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGCTG 660
QY 661 CAACCTGATGATGAAGAGTCCCTCCCTACCTTAATATATGATGATGATGATGATGATGAT 720
DB 661 CAACCTGATGATGAAGAGTCCCTCCCTACCTTAATATATGATGATGATGATGATGATGAT 720
QY 721 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
```

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QY 781 TGTGGATGTTGTTCTTTCTTAACACTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TGTGGATGTTGTTCTTTCTTTCTTAACACTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGAATGTGAACCAACAAAGTGAAGAAAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 CATGAATGTGAACCAACAAAGTGAAGAAAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 CGGTACCATGAACGGAAGAGATGATGAAGCCCTGTTGTTAACTTTCGAAGACAGCT 960
DB 901 CGGTACCATGAACGGAAGAGATGATGAAGCCCTGTTGTTAACTTTCGAAGACAGCT 960
QY 961 TCAGGCGACACAGTACTACACAGTTT 987
DB 961 TCAGGCGACACAGTACTACACAGTTT 987
```

RESULT 2
AAZ27916/C
ID AAZ27916 standard; DNA; 987 BP.

XX AAZ27916;

DT 20-DEC-1999 (first entry)

XX Complementary strand of canine B7-2 coding sequence.

KW B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; canine;

OS graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Canis familiaris.

PN WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

XX treating, e.g. autoimmune and atopic diseases -

XX Claim 1; Page 103-104; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)

XX encoding nucleic acid molecules from dogs and cats. The proteins can be

XX expressed by standard recombinant methodology. The nucleic acid molecules

XX and the encoded proteins can be used for preventing or treating diseases,

XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

XX development, graft rejection, inflammation, arthritic and atopic diseases

XX such as atopic dermatitis. They can be used in mammals such humans, dogs,

XX cats, cattle, sheep or pets. The products can also be used for detection,

XX diagnosis and drug screening.

XX Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Query Match 100.0%; Score 987; DB 20; Length 987;
Best Local Similarity 100.0%; Pred. No. 4.6e-287;

Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGTATCTCAGATGACACTATGGAACATTAACATTCTCTTTGTGATGACCCCTCGCTC 60
DB 987 ATGTATCTCAGATGACACTATGGAACATTAACATTCTCTTTGTGATGACCCCTCGCTC 928
```

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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 149.213 Seconds
(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-9

Perfect score: 987
1 atgattcagatgcactat.....acaacagctactacagttt 987

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	987	100.0	987	20	AAZ27915
2	987	100.0	987	20	AAZ27916
3	987	100.0	1897	20	AAZ27913
4	987	100.0	1897	20	AAZ27914
5	784.8	79.5	996	20	AAZ27931
6	784.8	79.5	996	20	AAZ27932
7	784.8	79.5	2830	20	AAZ27925
8	784.8	79.5	2830	20	AAZ27930
9	772.8	78.3	1080	21	AAZ34838

10	772.8	78.3	1080	21	AAZ34785	Cat CD86 (B7-2) CD
11	704	71.3	840	20	AAZ27923	Canine B7-2S prote
12	704	71.3	840	20	AAZ27924	Complementary stra
13	704	71.3	1795	20	AAZ27921	Canine B7-2S prote
14	704	71.3	1795	20	AAZ27922	Canine B7-2S prote
15	621	62.9	1050	21	AAZ49661	Pig costimulatory
16	575.2	58.3	1120	16	AAZ81351	Human B lymphocyte
17	575.2	58.3	1120	18	AAZ49181	Human B lymphocyte
18	575.2	58.3	1120	20	AAZ55784	Human B7-2 antigen
19	575.2	58.3	1120	21	AAZ84049	Human B lymphocyte
20	570.2	57.8	1424	21	AAZ29321	Human B7-2 cDNA
21	570.2	57.8	1428	16	AAZ85873	B70 type B antigen
22	570.2	57.3	2205	22	AAZ72616	Human cervical can
23	565.2	57.3	972	20	AAZ83208	B7-2 cDNA. Homo s
24	565.2	57.3	972	24	AAZ25510	Human co-stimulat
25	484.6	49.1	764	18	AAZ62939	Chimeric human/po
26	463.8	47.0	831	19	AAZ03230	DNA encoding CD86
27	453.8	46.0	738	20	AAZ80293	Human B7-2 extrac
28	453.8	46.0	738	22	AAZ89731	Nucleotide sequenc
29	369.8	37.5	509	20	AAZ27933	Feline B7-2 protei
30	369.8	37.5	509	20	AAZ27934	Feline B7-2 gene (
31	344.4	34.9	1151	20	AAZ55785	Mouse B7-2 antigen
32	344.4	34.9	1163	18	AAZ49182	Mouse B lymphocyte
33	344.4	34.9	1163	21	AAZ84050	Murine B lymphocyt
34	342.8	34.7	1163	16	AAZ81366	Murine B lymphocyt
35	337.2	34.2	1261	16	AAZ01046	Mouse B7-2 exons m
36	329.2	33.4	942	19	AAZ99926	Rat CD86 coding se
37	265.8	26.5	403	20	AAZ89569	EST clone CR506.
38	232.4	23.5	330	18	AAZ49197	Human B lymphocyte
39	232.4	23.5	330	21	AAZ84082	Human B7-2 variabl
40	218	22.1	450	21	AAZ00427	Human secreted pro
41	175.2	17.8	306	18	AAZ49198	Human B lymphocyte
42	175.2	17.8	306	21	AAZ84083	Human B7-2 constan
43	169.4	17.2	339	20	AAZ27935	Feline B7-2 protei
44	169.4	17.2	339	20	AAZ27936	Feline B7-2 gene (
45	103.4	10.5	210	16	AAZ01038	Human B7-2 exon 5.

ALIGNMENTS

RESULT 1	
AAZ27915	AAZ27915 standard; DNA; 987 BP.
ID	AAZ27915
AC	AAZ27915;
XX	
DT	20-DEC-1999 (first entry)
XX	
DE	Canine B7-2 protein coding sequence.
XX	
KW	B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis; ss.
KW	
XX	
OS	Canis familiaris.
XX	
PN	WO9947558-A2.
XX	
PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06187.
XX	
PR	19-MAR-1998; 98US-0078765.
XX	
PR	17-APR-1998; 98US-0062597.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Slim G, Yang S, Sellins KS;
XX	
DR	WPI, 1999-571822/48.
XX	
DR	P-PDB; AAY41076.
XX	

[illegible]

`/dev.stage="plasma cell leukemia"`
`/note="vector: lambda Zap Express; Site_1: EcoRI; Site_2:`
`XhoI; mRNA was purified from plasma cell leukemia`
`patient's peripheral blood containing >95% myeloma. An`
`oligo d(TT)18 primer containing XhoI restriction site was`
`used to prime first strand synthesis using M-MuLV reverse`
`transcriptase. To protect the cDNAs from XhoI digestion in`
`subsequent cloning step, the nucleotide analogue`
`5-methyl-dCTP was added to the nucleotide mixture and`
`a 32PldATP was added to monitor the quantity and quality`
`of first strand synthesis. After second-strand synthesis`
`and blunting of cDNA termini, EcoRI adapters were ligated`
`and followed by kinase treatment and digestion with XhoI.`
`The cDNAs were then size-fractionated using Sephacryl`
`S-500 column and then ligated into EcoRI and XhoI digested`
`lambda Zap Express vector. The ligation product was`
`packaged using Gigapack II packaging extract. The library`
`had primary titre of approx. 1x106. Clones from the`

primary library were randomly selected for single pass sequencing.

Query Match	10.6%	Score 104.2	DB 10	Length 314
Best Local Similarity	77.3%	Pred. No. 6.7e-17		
Matches 140; Conservative	0	Mismatches 38;	Indels 3;	Gaps 1;

Oy	14	GCACATATGGACCTGAATTAACATTTCTCTTTGGATGGACCTCCCTCTAAGGTCCTT	73
Db	125	GCACATATGGACCTAGTAACTTCTCTTTGGATGGCCCTTCCTCTCTGCTGCTCTT	184
Oy	74	CCATGAAAGAGTCAAGSCATATTTTCAACAAGACTGGAGACTGCCATTTTACAATTT	133
Db	185	CTCTGAGGATTAAGCTTATTTAATGAGACTC--AGACCTGCCCATTTGCAACT	241
Oy	134	CTCAAAACATTAAGCTTGGATAGTTGGTAGTGTTTGGCAGAGCCAGAGATTAAGCTGTTT	193
Db	242	CTCAAAACCAAAAGCCTGAGTAGTAGCTAGTATTTTGGCAGGAGCAAGAAAACTTGGTTC	301
Oy	194	T 194	
Db	302	T 302	

Search completed: October 20, 2002, 04:29:38
Job time : 1192.32 secs

QY	772	GCACATTTGTGGGATGGTGTGTTCTTTCTTACACACCTAAGGAAAAGGAAGAAAGCA---G	828
Db	516		1
QY	829	CCTGGCCCCCTCATCATGATGTGAACCAACAAGTGGAGAGAAAAGAAAGTGGACGACC	888
Db	456		1
QY	889	AAGGAAGAGTGTACCATGAAACGGGAACATCTGTATGAAGCCCACTGTG---TTAAC	945
Db	396		1
QY	946	ATTTCGAAGACAGCTTCAGCGACGAACAAGTACTACACAGTTT	987
Db	336	AGTTCGAAGACATCTTCATGCATCGACAAACAGTATCATATGTTT	295
LOCUS	AI093604/c		
DEFINITION	AI093604	570 bp	mRNA
ACCESSION	AI093604		
VERSION	AI093604.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Emmery, P.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 570)		
JOURNAL	NCI-CGAP		
COMMENT	http://www.ncbi.nlm.nih.gov/ncicgap.		
FEATURES	Unpublished (1997)		
source	Tumor Gene Index		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-rtelml.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Insert Length: 801		
	Seq primer: -40ml3 fwd. EST from Amersham		
	High quality sequence stop: 400.		
	Location/Qualifiers		
	1..570		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1634297"		
	/clone_id="Soares NSF_F8_9W_OT_PA_P_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site_1: Not I; Site_2: Eco RI;		
	Equal amounts of plasmid DNA from five normalized		
	libraries were mixed, and ss circles were made in vitro.		
	Following HAP purification, this DNA was used as tracer in		
	a subtractive hybridization reaction. The driver was		
	PCR-amplified cDNAs from pools of 5,000 clones made from		
	the same 5 libraries. The pools consisted of the following		
	libraries and cloneids: Soares NBHSF pool 1:		
	309384-310919, 323208-325855 Soares NB2HP pool 1:		
	145032-147355, 147720-148103, 148872-149255, 15002 -		
	150407, 151176-152327 Soares NB2HR8-9W pool 1:		
	758280-760583, 772104-774407 Soares NBHPA pool 1:		
	304776-306311, 320136-322823, 326280-326653 Soares NBHOF		
	pool 1: 723720-726407, 739080-740999 Subtraction by Bento		
	Soares and M. Fatima Bonaldo."		
BASE COUNT	150 a	107 c	134 g
ORIGIN	107 c	134 g	179 t
Query Match	10.8%;	Score 106.6;	DB 9;
Best Local Similarity	66.44;	Pred. No. 1, 9e-17;	Length 570;
Matches 184;	Conservative	0;	Mismatches 89;
			Indels 4;
			Gaps 2;
714	GAAGCCACCCCTGATGAGACACACATCCTCTGATTCGGGCTCTGCTTGTATGTTGCT	773	

Db	568	GCACCTCCACCTCC	CCCCGACACCATCTTGGATTACACTGACTCCAGCAGTTAT	509
Qy	774	CATTTTGTGTGGATGATGTCTTCTTCTTAACACTAAGAGAAAAGAGAAAGACAGCTGG	833	
Db	508	CATATGTGTGATGGTTCTCTGTCTGTCTATGCAAAATCGAAGAAAGAAAGAGGCGCTCG	449	
Qy	834	CCCCCTCATGATGATGTGAACCAACAAAGTGTGAGAGAAAAGAAAGTGTGACGACCAAGGA	893	
Db	448	CACCTCTATTAAATGTG-AACCAACACATATGTGAGGAGGGAAGAGGTGAACGACCAAGAA	390	
Qy	894	AAGAGTAGGATACCATGTAAGCAAGCAAGATGTGATGAACCCAGTGTG--TTAACAATTTTC	950	
Db	389	AAGAGAAAAAATTCATATACCTGAAAGATGTGATGAAACCAACGCGTGTGTTTAAAGTTTC	330	
Qy	951	GAGACACGCTTCAGCGCAGCAACAGTACTACACAGTTT	987	
Db	329	GAAAGACATCTTCATGCGACAAAGATGATCATGTGTTT	293	
RESULT 14				
AA946810/c				
LOCUS	AA946810	504 bp	mRNA	linear EST 23-JUL-1998
DEFINITION	oq33c01.s1 NCI_CGAP_Kid5 Homo sapiens CDNA clone IMAGE:1589088 3'			
	similar to SW:CB86.HUMAN P42081 T LYMPHOCTE ACTIVATION ANTIGEN			
	CD86 PRECURSOR ; , mRNA sequence.			
ACCESSION	AA946810			
VERSION	AA946810.1	GI:3110205		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 504)			
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
TITLE	National Cancer Institute, Cancer genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index			
COMMENT	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.			
	Emmert-Buck, M.D., Ph.D.			
	CDNA Library Preparation: M. Bento Soares, Ph.D.			
	CDNA Library Arrayed by: Greg Lennon, Ph.D.			
	Clone Sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: NCI-CGAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	www-bio.llnl.gov/bdrrp/image/image.html			
	Insert length: 1276 Std Error: 0.00			
	Seq primer: -40m13 fwd. ET from Amersham			
	High quality sequence stop: 457.			
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	/clone="IMAGE:1589088"			
	/clone_1lb="NCI_CGAP_Kid5"			
	/tissue_type="2 pooled tumors (clear cell type)"			
	/lab_host="DH10B"			
	/note="Organ: Kidney; Vector: pUT3D-Pac (Pharmacia) with			
	a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st			
	strand cDNA was primed with a Not I - oligo(dT) primer [5'			
	AACGTGACAGATTCGCGCGCGCAATATTTTTTTTTTTTTTTTTTTT 3'],			
	double-stranded cDNA was ligated to Eco RI adaptors			
	(Pharmacia), digested with Not I and cloned into the Not I			
	and Eco RI sites of the modified pUT3 vector. Library			
	went through one round of normalization. Library			
	constructed by Bento Soares and M. Fatima Bernaldo. "			
BASE COUNT	136 a	94 c	109 g	165 t
ORIGIN				
Query Match	10.6%;	Score 104.8;	DB 9;	Length 504;
Best Local Similarity	76.5%;	Pred. No. 5.4e-17;		

QY	924	TGATGACCCGAGCTG---TTAACTTTCGAAGACAGCTTCAGCGCAACAGTACTAC	980
Db	313	TGATGACCCGAGCTGTTTAAAGTTTGAAGACATCTTCATCGACAAAGTGATAC	372
QY	981	ACAGTTT	987
Db	373	ATGTTT	379
RESULT	11		
LOCUS	BG001664	347 bp	mRNA linear
DEFINITION	RC4-GN0067-151100-016-b07 GN0067	Homo sapiens	CDNA, mRNA sequence.
ACCESSION	BG001664		
VERSION	BG001664.1	GI:12440219	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 347) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496 (2000)
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-GN0067-151100-016-b07&t3=2000-11-15&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 347. Location/Qualifiers 1..347 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="GN0067" /dev_stage="Adult" /note="Organ: Placenta,normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	109 a	75 c	75 g
ORIGIN			88 t
Query Match	12.7%	Score 125.6;	DB 10; Length 347;
Best Local Similarity	6.6%	Pred. No.1.5e-22;	
Matches 231; Conservative	0;	Mismatches 86;	Indels 12; Gaps 4
QY	638	ATGTGACATCTTCGTGTCTGTCGCAACTGAGTCAATGAGTCTCCCTCCCTACCTTANA	697
Db	21	ATGTGACATCTTCGTGTATCTGTAAGACGCAAGCGCGTTTATCTTCATCTTCCT	80
QY	698	ATATGATGACATATGCAAAACCCACCCCTGAGTGAGACCAATCTCTTGATTCGCGCTC	757

DB	81	CTACAGA---GOTTAAAGACCCCTCAGCCCTCCGCCAGACCAACATTCCTTGATTAACAGCTG	137
OY	758	TGCTTGTAATGTGGTCAATTTGTGTGGAGTGTCTTTCTTAACACTAAGGAAA---A	814
Db	138	TACTTCCACACA---GTTATTATATGTGAGTGAGTGTCTTGTCTTAATCTATGAGGAATGA	194
OY	815	GGAAGAAAGACAGCGCTGGCCCTCTCATGTGATGTGAACAACCAACAGTGGAGAGAAAAG	874
Db	195	AGAAGAAAGACAGCGCTGGCACTCTTATTAATGTGTGGAACCAACACATGTGAGAGGAAAG	254
OY	875	AAATGACACAGACCAAGAAAAGTAGCGGTACATGAAACGGAAGAATCTGATGAAGCCC	934
Db	255	AGAGTGAACAGACCCAGAAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCC	314
OY	935	AGTGTG---TTAACATTTTCGAAGACAGCGCTCA	963
Db	315	AGCGTGTTTTAAAGTTTCGAGAGACATCTTCA	346
RESULT 12			
LOCUS	BF064222/c		
DEFINITION	BF064222	543 bp	linear EST 16-OCT-2000
LOCUS	7357b02.x1 Soares_NSF_F8_9W_OT_PA_P_S1		Human sapiens CDNA clone
DEFINITION	IMAGE:3390507 3	Similar to SW:CD86.HUMAN P42081	T LYMPHOCYTE
ACCESSION	BF064222		ACTIVATION ANTISEN CD86 PRECURSOR ; , mRNA sequence.
VERSION	BF064222.1	GI:10823132	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 543)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: c9apbs-r@mail.nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Seq primer: -40UP from Gibco		
FEATURES	High quality sequence stop: 496.		
Source	Location/Qualifiers		
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	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Equal amounts of plasmid DNA from five normalized		
	libraries were mixed, and ss circles were made in vitro.		
	Following HAP purification, this DNA was used as tracer in		
	a subtractive hybridization reaction. The driver was		
	PCR-amplified cDNAs from pools of 5,000 clones made from		
	the same 5 libraries. The pools consisted of the following		
	libraries and clones: Soares NBHSF pool 1:		
	309384-310919, 323208-325895 Soares NB2HP pool 1:		
	145032-147335, 147720-148103, 148872-149255, 15002 -		
	150407, 151176-152327 Soares NB2HF8-9W pool 1:		
	758807-760583, 772104-774407 Soares NBHPA pool 1:		
	304776-306311, 320136-322823 326280-32663 Soares NBhOT		
	pool 1: 723720-726407, 739080-740939 Subtraction by Bence		
	Soares and M. Fatima Bonaldo."		
QUERY COUNT	151 a	104 c	112 g 175 t 1 others
ORIGIN			
Query Match	11.8%	Score 116.4	DB 10; Length 543;
Best Local Similarity	76.6%	Pred. No. 4.7e-20;	
Matches 170; Conservative	0;	Mismatches 46;	Indels 6; Gaps 2;

[illegible]

OY	352	AAGGACTCGTTCCA	367
Dd	242	CACGATTGGTTCGA	257
RESULT 10 AM516826			
LOCUS	AM516826		
DEFINITION	AW516826	496 bp	mRNA linear EST 03-MAR-2000
	xqy04h01.xl Soares_NHCEC_cervical_tumor Homo sapiens CDNA clone		
	IMAGE:2748913_3 similar to SW:CD86_HUMAN P42081 T LYMPHOCTE		
ACCESSION	AW516826		
VERSION	AM516826.1	GI:7154992	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
AUTHORS	Tumor Gene Index		
TITLE	Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgaaps-remail.nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (infoimage.lnl.gov) for further information.		
	Possible reversed clone: similarity on wrong strand		
	Seq primer: -40UP from Gdbco		
	High quality sequence stop: 458.		
FEATURES	Location/Qualifiers		
SOURCE	1..496		
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	/lab_host="DH10B (phage-resistant)"		
	/note=Organ: cervix; Vector: pTV3D-Pac (Pharmacia) with		
	a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st		
	strand cdna was primed with a Not I - oligo(dty) primer [5'		
	TGTACCATCTCAAGTGAGGAGCCGCCGCAGAGTTTTTTTTTTTTTTTTT		
	T 3']: double-stranded cdna was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pTV3 vector.		
	Llibrary is normalized; constructed by Bento Soares and		
	M.Patrina Bonaldo."		
BASE COUNT	156 a	102 c	93 g
ORIGIN			145 t
Query Match 14.7% : Score 144.6; DB 9; Length 496; Best Local Similarity 69.8%; Pred. No. 1.ee-27; Matches 256; Conservative 0; Mismatches 99; Indels 12; Gaps 4;			
OY	627	TGAAGCACCATGTGACACATCTTCTGTGTGCTCCTGACAATTGATGAAAGCTTCCCTC	686
Dd	19	TGTTAGCGCAAATGACCACTTCTGTATTTCTGAAAATGACAAAGCGGCTTTATC	78
OY	687	CCTAAGCTTAATAATAGATGACATFAGAANAACCCAGCCCGATGAGAACCAACATCTCTG	746
Dd	79	TTTCACTTTTCTCTATGAG--CTTGAGAGACCTTCAGCTCCCCAACAACATCTCTTG	135
OY	747	GATTGGCGCTCTGCTTGAATGTGTGATCTTTTGTTGGATGGTGTCTTCTTAACACT	806
Dd	136	GATTACAGCTGTACTTCCACA---GTTATTATATGTGTATGTTCTTGCTTAATTCT	192
OY	807	AAGGAAA----AGGAAGAAGACAGCTTGGCCCCTTCATGATGTGAAAAACAACAAAGT	863
Dd	193	ATGGAATGMAAGAAAGAAAGCGCTCCGCACTTAAATAAGTGTGAACACAACAAT	252
OY	864	GGAGAGAAAAGAAAGTACAGACCAAGGAAAAGTACGGTACATGATAAAGCAACATAC	923
Dd	253	GGAGAGGGAAGNGTADACAGACCAAGAAAAGGAAAATAATCAATVACCTGAAGATC	312

QY	610	TTGTCTCTTCAGTCCCGGAAAGCAGCAATGAGACATCTTCTGTCTCTCAACTTTAG	669
Db	339	GTGTCTCTTCCATCCCTCCCGAGACAATATGAGCAGCATGTGTGTCTTCCAACTTTAG	334
QY	670	TCAAAGGAA-----GCTTCCCTCCCTACCTTATATATATAGATGCA---CATACGAAAGCC	720
Db	333	CCAAACGAGACACCTGCTTTTCTCCCTACCTTATATATAGATGCAAGCACCTGTGCA	274
QY	721	ACCCCTGATGAGACACCATCTCTGATTTGGGGCTCTGCTTTGATATGTCATTTTG	780
Db	273	CCCCCTGTCGCCAGACCATCTCTTNGATTTGAGCTTACTTTGATACAGTGGTCTGTG	214
QY	781	TTGTGGGATGCTCTTCTTCTTAACACTAAGAAAGAAAGAACACCCTGGCCCTCT	840
Db	213	TTGTGGGATGCTCTTCTTGTAACTAAGAAAGAAAGAAAGAACACCCTGGCCCTCT	154
QY	841	CATGAAT---GTGAAGAACCAACAACTGTGAGAGAAAGAAAGAAAGTGAAGACCAAGAAAGA	897
Db	153	AATGAATGTGTGGAACCATCAATATGAACAGAGAGGAGATGAAACAACTRAAGACAGA	94
QY	898	GTACGGTACCATGAAAGGAAAGATCTGATGAAGCCCACTG---TGTTAAGATTTTGAAG	954
Db	93	AGTCAT-----GAAAGATCTGATGATGCCAGTGTGATGATTAATATTTTNAAG	45
QY	955	ACAGCTCAGGCGACACAGTACTACTACAGATTT	987
Db	44	ACAGCTCAGATGACACACAGTACTACTACATTTT	12
RESULT 8			
LOCUS	BB635605	654 bp	mRNA
DEFINITION	BB635605	RIKEN full-length enriched, 0 day neonate thymus Mus	
ACCESSION	BB635605	musculus cDNA clone A430076L06 5', mRNA sequence.	
VERSION	BB635605.1	GI:16471650	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1 (bases 1 to 654) Arkawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Arkawa,T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) waghi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Itawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)		

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamane, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.ysc.riken.go.jp>) for further details.
 e mouse tissues.
 Location/Qualifiers
 1. 654
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 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site:1: Sali; Site:2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGACGCTCTTTTGTGATGACCCCTGCTATGAGTGGTCT 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGTAGTATTAATTAATTCACCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda ϕ C119.
 BASE COUNT 148 a 151 c 152 g 202 t 1 others
 ORIGIN
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 Best Local Similarity 71.0%; Pred. No. 4,2e-43;
 Matches 269; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
 13 TGCATATGGAACCTAATAACATCTCTCTTTGGATGACCCCTGCTATGAGTGGTCT 72
 276 TGCACCATGCGCTTGCGCAATCTTATCTTTTGACAGCTTCGTATGATGCATGCTTT 335
 73 TCCATGAAGAGTCAGACATATTTCACAAGACTGAGACTGCCATTTTACAAT 132
 336 TCCGCGAGACSCAGCTTATTTCATGGAGTCGATVCTGCCCTGCCATTTACAAG 395
 133 TCTCAACATATAGCTCGATGATGTTGTGATGTTTGGACGACCAAGATACTGGTT 192
 396 GCTCAAAACATAGCCTAGTAGTGCTGTGATTTTGGCAGGACACCAAAAGTTGGTT 455
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 313 AAGGCTGTATCATGTTGCTTATCATATATAAGGCCCCCAAGAGCATGTCCTCCATGCAC 372
 576 ATGGGCTGTATGATTTGTTTATACAAAAAAGCACCACAGCATCAATTATCCTCCA 635
 CAGATGAATTCTGACCTAT 391

QY 598 GTTCTATCAGCTTGTCTTCAGTCCCTGAG 631
 DB 663 ATCTCCACAGGCTCTCTTTCATTCGCGATG 696

RESULT 6
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 LOCUS 503647 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM089797
 VERSION BM089797.1 GI:17000425
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 578)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perleza,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keeler,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.
 PCR primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCAGCAGC
 Plate: 5 row: D column: 18
 Seq primer: ATTAGTGACACTATAG.
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 /tissue_type="pooled"
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 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."
 BASE COUNT 170 a 150 c 120 g 137 t 1 others
 ORIGIN

Query Match 26.1%; Score 257.2; DB 10; Length 578;
 Best Local Similarity 76.9%; Pred. No. 2.6e-57;
 Matches 349; Conservative 0; Mismatches 83; Indels 22; Gaps 2;

QY 1 ATGTATCTCAGATGACATGGAATAACATCTCTTGATGATGACCTCCTGCTC 60
 DB 124 ATGCGTTTCAATGACCATGGGACTGCGAAACACTCTATATGATGCGCTCCTGCTC 183
 QY 61 TAT-----GTTGCTGCTTCAT-GAAGAGTCAAGCATATTTCAA 98
 DB 184 TCTGTTCCACGTCTCTTTTCAGGTGCTGCTTCTTGAAAGTCAATGCTTTTAA 243
 QY 99 CAAGACTGGAGACTGCCATTTTCAAAATTCGAAACATTAAGCTGGATGACTT 158
 DB 244 CGAGACTGGAGAACTGCATGCTTTCAAACACCAAAACCTCAGCTGGAGACT 303
 QY 159 GGTACTGTTTTGGCAGACGACGATTAAGCTGTTCTGTACGAGCTATACAGAGCAAGA 218

DB 304 GGTATATTTTGGCAGGATCAGAAATAGTTGTTCTATAGCTATTAATCAAGCCAGA 363
 QY 219 GAGCCCTCAAAATGTTTCATGCGAAGTATTAAGGGCGGACAAAGCTTGCACAAAGCAATTG 278
 DB 364 GAGCCCAATATATGTTATTCCTCCAAAGTATTAAGGGCGGACAAAGCTTGCACAGGACACTTG 423
 QY 279 GACCTGAGACTCCATATATTTAGATCAAGACAGAGGCTTTATCAATGTTTCGTTCA 338
 DB 424 GACCTTGAGACTCCACAAAGCTTCAATCAAGACAGAGGCTGATCAATGTTTCATCA 483
 QY 339 TCATTAAGGGCCCAAGAGACTTCGTCATGACCAAGCAATGATTAATTTACTATCAGTGT 398
 DB 484 TCATTAAGAGGTCCTCCAGAGATTGTTTCATCCACAGATGATGTTGACCTGATAGTGT 543
 QY 399 TGCTAATCTCAGTCACACTGGAATATATGTTACT 432
 DB 544 GGCTAATCTCAGTCACACAGAAATTAAGCTAAT 577

RESULT 7
 AA056905/c 512 bp mRNA linear EST 18-SEP-1996
 LOCUS EST224F Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)
 DEFINITION Sus scrofa cDNA clone SPL224 forward similar to L25259 CTUA4
 counter-receptor , human, mRNA sequence.
 AA056905
 AA056905.1 GI:1549545
 EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 512)
 Tuggle,C.K., Wahls,S. and Schmitz,C.
 Expresed Sequence Tags from Pig Spleen
 Unpublished (1996)
 CONTACT: Tuggle CK
 Molecular Genetics Laboratory, Department of Animal science
 Iowa State University
 201 Kildee Hall, Ames, IA 50011-3150, USA
 Tel: 5152944252
 Fax: 5152942401
 Email: cktuggle@iastate.edu
 PCR primers
 FORWARD: TGGCGAGACTCCTG
 BACKWARD: GACCGGCTCAGCT
 Insert length: 950 Std Error: 50.00
 Seq primer: TGGCGAGACTCCTG.
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 source location/Qualifiers
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 # PL1006b)"
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 /note="oligo (at) primed"
 BASE COUNT 125 a 106 c 114 g 163 t 4 others
 ORIGIN

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 Matches 387; Conservative 0; Mismatches 99; Indels 27; Gaps 6;

QY 490 TACCACAAACCCAGAGATGATTTTGTGTAACCAAGCAATTAAGTACTAAGTAT 549
 DB 512 TACCAGAAACCCAGAGATGATATGTTCTTAATCGAAGATTCACACACTGAGCAT 453
 QY 550 GATCTGTCATGAAGAATCTCAAAATTAATGTCACAGAACTTACAAAGTTTATACAG 609
 DB 452 GATCTGACATGAAGAATCTCAAAATTAATACATCAG-6GANTTTACATGATATCAATCAGG 394


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AA056906      448 bp      mRNA      linear      EST 18-SEP-1996
LOCUS          AA056906
DEFINITION     EST224R Pig Spleen lambda gt 11 library (Clontech Cat # PL1006b)
               Sus scrofa cDNA clone SPL224 reverse similar to L25259 CTL4A
               counter-receptor, human, mRNA sequence.
ACCESSION      AA056906
VERSION        AA056906.1
KEYWORDS       GI:1549546
SOURCE         EST.
ORGANISM       Sus scrofa
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE      1 (bases 1 to 448)
AUTHORS        Tuggle,C.K., Wahls,S. and Schmitz,C.
TITLE          Expressed Sequence Tags from Pig Spleen
JOURNAL        Unpublished (1996)
COMMENT        Contact: Tuggle CK
               Molecular Genetics Laboratory, Department of Animal Science
               Iowa State University
               201 Kildee Hall, Ames, IA 50011-3150, USA
               Tel: 5152944252
               Fax: 5152942401
               Email: cktuggle@iastate.edu
               PCR Primers
               FORWARD: TGCGGACGACTCTG
               BACKWARD: GACCGGCGTCAGCT
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Db 1 CTCGTGGGATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
OY 96 CACCAAGACTGAGAACTGCGCATGCCATTTTACAAATTTCTCAAAACATTAAGCTGATGA 155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CAATAGACTGAGAACTGCGCATGCCATTTTACAAACCTCGAAGACCTGATGA 120
OY 156 GTTGTAGTGTGGGAGGACAGATAGCTGTTCTGTACGAGCTATACAGAGCAA 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GCTGTCAATTTTGGAGAGACAGATACCTGTTCTCTCAACGATATCGAGGCCA 180
OY 216 AGAAGACCTCAAAATGTTCAATCGCAATATAGGGCGCACAAAGCTTGACAAAGACAA 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGAGAAGCTCATATATGTTAATTCACATATATGGTGTGACAAAGCTTGACAGGCCAC 240
OY 276 TTGACCTGAGACTCCATTAATATTCAGATCAAGACAAAGGGCTTGATCAATGTTTCGT 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CTGACCTGAGACTCCCAACAGCTCAATCAAGACAAAGGGCTCATCATGTTTCAT 300
OY 336 TCATCATAAAGGGCCCAAGAGACGTCGCCATGACAGACAGATGTAATTCGACCTATAGT 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 CCATCATAAAGGGCCGACAGATGATGTCCTATCCACAGATGATGCTGACCTATAGT 360
OY 396 GCTTGTCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GCTTGTCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 419

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OY 456 CATCATAAATTTGACCTGCTCATCATACACAA 486
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Db 420 --TCATAAATTTGACCTGCTCATCATACACAA 448

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DEFINITION   BB631711 RIKEN full-length enriched, 16 days neonate thymus Mus
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ACCESSION    BB631711
VERSION      BB631711.1
KEYWORDS     GI:16468418
SOURCE       EST.
ORGANISM     Mus musculus
               house mouse.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 629)
REFERENCE     1
AUTHORS       Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
               Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
               M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
               Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
               D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
               Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
               Muramatsu,M. and Hayashizaki,Y.
               RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
               Unpublished (2001)
               Contact: Yoshihide Hayashizaki
               Laboratory for Genome Exploration Research Group, RIKEN Genomic
               Sciences Center(GSC), Yokohama Institute
               The Institute of Physical and Chemical Research (RIKEN)
               1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
               Tel: 81-45-503-9222
               Fax: 81-45-503-9216
               Email: genome-res@gsr.riken.go.jp,
               URL: http://genome-gsc.riken.go.jp/
               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
               M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
               Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new
               genes. Genome Res. 10 (10), 1617-1630 (2000)
               wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
               Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
               S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
               Hayashizaki,Y.
               RIKEN integrated sequence analysis (RISA) system--384-format
               sequencing pipeline with 384 multicapillary sequencer. Genome Res.
               10 (11), 1757-1771 (2000)
               Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
               Y. and Hayashizaki,Y.
               Computer-based methods for the mouse full-length cDNA
               encyclopedia: real-time sequence clustering for construction of a
               nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
               Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaoka,I., Aizawa
               K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
               Hayashizaki,Y.
               Computational Analysis of Full-Length Mouse cDNAs Compared with
               Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
               Please visit our web site (http://genome-gsc.riken.go.jp) for
               further details.
               e mouse tissues.

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FEATURES

source

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1176.32 Seconds

(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-9

987

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scoring table:

13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: em_gss_inu:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	358	36.3	655	10	BI824940 603032554
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4	281.4	28.5	629	9	BB631711 BB631711
5	263.2	26.1	1002	10	BF137460 601780644
6	257.2	26.1	578	10	BM089797 503647 MA
7	243	24.6	512	9	AA056905 EST224F P
8	203.6	20.6	654	9	BB635605 BB635605
9	176	17.8	257	9	AA427922 64549 MAR
10	144.6	14.7	496	9	AA516826 xg04h01 x
11	125.6	12.7	347	10	BC001664 KC4-GN006
12	116.4	11.8	543	10	BF064222 7157B02.x
13	106.6	10.8	570	9	AI093604 ou82b09.s
14	104.8	10.6	504	9	AA946810 Cq43C01.s
15	104.2	10.1	314	10	BF171298 PCL2416 M
16	99.2	8.2	480	9	AW260541 um83a03.y
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18	72.4	7.3	133	10	BF925793
19	72.4	7.3	156	10	BF925798
20	57.2	5.8	486	10	BI132458 AR031A11L
21	50	5.1	695	10	BI767024 603054234
22	49	5.0	1101	12	CNS0039G
23	45	4.6	391	9	AI632116
24	43	4.4	378	9	AA973387
25	39.6	4.0	1032	10	BI762625
26	39	4.0	1571	10	BE622476
27	38.6	3.9	483	10	N93892
28	38.4	3.9	523	12	AC0830201
29	38.2	3.9	317	9	BI125839
30	38.2	3.9	477	12	A2460082
31	38	3.9	454	10	BF089036
32	38	3.9	537	12	AO665728
33	38	3.9	693	12	BH577208
34	38	3.9	735	12	BH595210
35	38	3.9	893	12	BH157217
36	37.8	3.8	634	10	BS986969
37	37.8	3.8	725	9	AU120535
38	37.6	3.8	404	9	AA934109
39	37.6	3.8	868	12	BH150993
40	37.6	3.8	936	12	BH138103
41	37.6	3.8	952	12	A2673595
42	37.4	3.8	472	10	W79680
43	37.4	3.8	528	10	BE501884
44	37.4	3.8	635	9	AA186324
45	37.4	3.8	701	10	BC620142

ALIGNMENTS

RESULT 1
BI906246 753 bp mRNA linear EST 16-OCT-2001
DEFINITION 603063172P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212648 5',
LOCUS BI906246
ACCESSION BI906246
VERSION BI906246.1 GI:16168907
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM11533 row: 0 column: 17
High quality sequence stop: 719.
Location/Qualifiers
1..753
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5212648"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV
(destroyed); RNA source: leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

[illegible]

BASE COUNT	354 a	237 c	230 g	299 t	
Query Match	58.3%;	Score 575.2;	DB 6;	Length 1120;	
Best Local Similarity	77.8%;	Pred. No. 6.7e-144;			
Matches 775; Conservative	0;	Mismatches 203;	Indels 18;	Gaps 6	
QY	1	ATGTAATCTAGATGACGCTTGGAACGATGATTAACATCTCTTTGTGATGACCCCTGCTC	60		
DB	107	ATGGATCCCAATGACGATGACGATGAGACGATGATACATCTCTTTGTGATGCGCTTCCTGCTC	166		
QY	61	TATGTCGTCTGCTCCATGAGAGTCAAGCATATTTCCACAAGACTGGAACTGGCATC	120		
DB	167	TCTGGTGGCTGCTCCCTGCTGAGATTTCAAGCTTTTTCAAAGAACTGCAACCTGGCATC	226		
QY	121	CATTTTACAAATTCCTCAAAACATTAACCTCGATGAGTGTGTGTGGAGACACAG	180		
DB	227	CATTTTGCACAACTCTCAAAACCAAGCCCTGAGTGAAGTATTTTGGAGAGACAG	286		
QY	181	GATTAAGCTGTTCTGTACGACTATACAGAGGCAAGAGAACCCCTCAAAATGTTCTCGC	240		
DB	287	GAAACTTGTCTGTGATGAGATGATCTTATAGGCAAAAGAAATTTGACAGTGTCTATTC	346		
QY	241	AAGTAAAGGCGCGCAGCGCTTGGCAAAAGCAATTTGGACCTGAGCTCCATATAT	300		
DB	347	AAGTATATGGCGCGCAAGATTTGATTGGAGAGTTGGACCTGAGACTTCACAACTTT	406		
QY	301	CAGATCAAGAGCAAGGCGTTGATCTATGTTTCGTCATCATTAAGGGCCCAAGGACTC	360		
DB	407	CAGATCAAGAGCAAGGCGTTGATCTATGATCATTCATCCACAAAAGCCACAGGAATG	466		
QY	361	GTTCCCATGACCAAGATGATTTCTGACCTATCAGTCTTGTCTACTTCAGTCAACCTGAA	420		
DB	467	ATTGCGATCCACAGATGATTTCTGACGTCGCTCTGCTATCTTCACTTCACTGAA	526		
QY	421	ATATGCTACTCTCTATATGAACAGAAAAATTCGGCATATATAATTTGACCTGCTATCC	480		
DB	527	ATAGTACCAATTTCTATATTAACAGAAAA--TGTGACATTAATTTGACCTGCTCATCT	583		
QY	481	ATACAAGTTACCAGAACCCCAAGAGATGATTTTTTGTAAAAAACGAGAAATTCACT	540		
DB	584	ATACAGGTTACCACCAAGACCTTAAGAAATGAGTGTGTTGTAAGAACCAAGAAATTCACT	643		
QY	541	ACTAATGATGATCTGTCATGAAAGAAATCTCAAAATATCTCAGAGACTCTCAACGTT	600		
DB	644	ATGAGATATGATGATTTATGACAAATCTCAAGATATATCTCAGAGACTCTCAACGTT	703		
QY	601	TCTATCAGCTTGTCTTCTCAGTCCCTGAAG--CAAGCAATGTGAGCATCTTCTGTCTC	657		
DB	704	TCCATCAGCTTGTCTTCTTCTATTCCTGATGTACGAGCAATATGACCATCTTCTGATTT	763		
QY	658	CTGCACTTGAGTCATGAAAGCTTCCCTCCCTACCTATATATATAGTGCACATACGAA	717		
DB	764	CTGGAAGCTTGCACAAAGCGCGCTTTATCTTCTCACTCTCTCTATAGA--GCTTGAGAGAC	820		
QY	718	CCGACCCCTGATGAGAACACCATCTCTGATGTCGCGCTGCTGTATATGTTGTCATT	777		
DB	821	CTTACAGCTTCCCGACAGCCACATTTCTTGATTAACAGCTTACTTCCAA--CAGTATAT	877		
QY	778	TGTGTGGGATGTTGTTCTTTTAACACTTAAGAAA--AGAAAGAAAGACGCGCTGCG	834		
DB	878	ATATGCTGATGTTCTTCTGCTCTAATTTCTTGAAGAAAGAAAGAAAGCGCGCTGCG	937		
QY	835	CCCTGCTCAATATGTAAGAACCAACAAAGGTGAGAGAAAGAAAGTGTGACAGCAAGAA	894		
DB	938	AACCTTATTAATGATGAGAACCAACACATATGAGAGGAAAGAGAGTGAACAGCAAGAA	997		
QY	895	AGAGTACGATACCATGAAGCGAAAGATCTGATGAAGCCAGTGTG--TTAACTATTG	951		
DB	998	AGAGAAAAAATTCATATACCTGAAGAGATCTGATGAAGCCAGCGTGTTTTAAAGATTG	1057		
QY	952	AGACAGCTTCAGGCGCAACAGTACTACACAGTTT 987			

Db 878 ATATGTGATGTTTCTTCTCTAATTCATGAAATGGAAGAGAGAGCGCTCCG 937
Qy 835 CCCTCTCATGATGTGAAACCAACCAAGTGGAGAGAAAGAGTACAGACCAAGAA 894
Db 938 AACCTCTTAATGATGGAACCAACCAATGGAGAGAGAGAGAGACCAAGAA 997
Qy 895 AAGATGACGTACCAAGAGAGAGAGATGTGATGAGCCAGCTGTG---TTAACATTTG 951
Db 998 AAGAGAAAATCCATATACCTGGAAGATCTGATGAAGCCAGCGTCTTTTAAAGTTG 1057
Qy 952 AAGACAGCTTCAGGAGAGAGAGAGTCTACAGCTT 987
Db 1058 AAGACATCTTCATGCGAGAGAGATATACATGTTT 1093

RESULT 12
LOCUS AR030780 1120 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5861310.
ACCESSION AR030780
VERSION AR030780.1 GI:5943994
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 1120)
TITLE Freeman,G.J., Nadler,L.M. and Gray,G.S.
Tumor cells modified to express B7-2 with increased immunogenicity
and uses thereof
JOURNAL Patent: US 5861310-A 1 19-JAN-1999;
FEATURES
source Location/Qualifiers
1..1120
/organism="unknown"

BASE COUNT 354 a 237 c 230 g 299 t
ORIGIN

Query Match 58.3%; Score 575.2; DB 6; Length 1120;
Best Local Similarity 77.8%; Pred. No. 6,7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

Qy 1 AATGATCCAGATGACATGATGAGAGTGAATACATCTCTTGTGATGAGCCCTGCTC 60
Db 107 AATGATCCAGATGACATGATGAGAGTGAATACATCTCTTGTGATGAGCCCTGCTC 166
Qy 61 TATGTCGTCTTCATGATGAGAGTGAATGATGATTCATGATGAGAGTGAATGATG 120
Db 167 TCTGGTGTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 226
Qy 121 CATTTTCAAAATTCGAAACATTAAGCCTGATGATGATGATGATGATGATGATG 180
Db 227 CAATTTGCAAACTCTCAAAACCAAGCCTGATGATGATGATGATGATGATGATG 286
Qy 181 GATTAAGCTGTCTCTGATGAGAGTATGAGAGGAGAGAGAGAGAGAGAGAGAGAG 240
Db 287 GAAAACTGTGTTCTCAATGAGGTATGATGAGAGAGAGAGAGAGAGAGAGAGAG 346
Qy 241 AAGTAAAG 300
Db 347 AAGTAAAG 406
Qy 301 CAGATCAAG 360
Db 407 CAGATCAAG 466
Qy 361 GTTCCAGTCCAG 420
Db 467 ATTCCAGTCCAG 526
Qy 421 AATTAAGTAACTCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 527 AATTAAGTAACTCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
Qy 481 AATTAAGTAACTCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Db 584 ATACACGTTTACCCAG 643
Qy 541 ACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 644 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
Qy 601 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
Db 704 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
Qy 658 CTGCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
Db 764 CTGCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 820
Qy 718 CCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 777
Db 821 CCTGAGCTCCCGAG 877
Qy 778 TTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
Db 878 ATATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937
Qy 835 CCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
Db 938 AACCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Qy 895 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
Db 998 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
Qy 952 AAGACAGCTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
Db 1058 AAGACATCTTCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1093

RESULT 13
LOCUS AR112747 1120 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6130316.
ACCESSION AR112747
VERSION AR112747.1 GI:14092647
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 1120)
TITLE Freeman,G.J., Nadler,L.M., Gray,G.S. and Greenfield,E.
Fusion proteins of novel CTLA4/CD28 ligands and uses therefore
JOURNAL Patent: US 6130316-A 1 10-OCT-2000;
FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 354 a 237 c 230 g 299 t
ORIGIN

Query Match 58.3%; Score 575.2; DB 6; Length 1120;
Best Local Similarity 77.8%; Pred. No. 6,7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

Qy 1 ATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Db 107 ATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 166
Qy 61 TATGTCGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 167 TCTGGTGTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 226
Qy 121 CATTTTCAAAATTCGAAACATTAAGCCTGATGATGATGATGATGATGATGATG 180
Db 227 CAATTTGCAAACTCTCAAAACCAAGCCTGATGATGATGATGATGATGATGATG 286
Qy 181 GATTAAGCTGTCTCTGATGAGAGTATGAGAGGAGAGAGAGAGAGAGAGAGAGAG 240

RESULT 9
LOCUS ARI59758 1002 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 33 from patent US 6251627.
ACCESSION ARI59758
VERSION ARI59758.1 GI:16222530
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6251627-A 33 26-JUN-2001;
FEATURES
Source location/Qualifiers
1..1002
BASE COUNT 309 a 215 c 203 g 275 t
ORIGIN

Query Match 58.3%; Score 575.2; DB 6; Length 1002;
Best Local Similarity 77.8%; Pred. No. 6.7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

OY 1 ATGATCTCAGATGCACTATGAACTGAATAACATTTCTTTGTGANGACCCCTGCTC 60
DB 7 ATGATCCCCAGTGCACTATGGAAGTGAACAATTCCTTTGTGATGGCCTTCTGCTC 66
OY 61 TATGCTGCTGCTCCATGAAAGTCAAGCATTTTCAACAAGACTGGAGAAGCTCCATGC 120
DB 67 TCTGTTGTGCTCTCTCTCAATGATTCACATTTTTCATGAGCTGACAGACCTCCATGC 126
OY 121 CATTTTAAATAATTCCAAAACATTAAGCCTGGATGAGTGGTGTGTTTGGCAGACCAAG 180
DB 127 CAATTTGGAACCTCTCAAAACCAAGCCTGAGTGAGCTAGTAGTATTTTGGCAGGACCAAG 186
OY 181 GATAAGCTGTTCTGTACAGCTATACAGAGGCAAGAAAGCCCTCAAAATGTTCTATGC 240
DB 187 GAAACCTGTTCTGATGATGAGTATCTTAGGCAAGAAAGATTTGACAGTTCATTTCC 246
OY 241 AAGTTAAGGGCCGACAGCTTTGACAAAGCAATTTGGACCTTGAGACTCCATTAATTT 300
DB 247 AAGTTAAGGGCCGACAGCTTTGATTCGAGCAAGTTGGACCTTGAGACTCCATTAATTT 306
OY 301 CAGATCAAGGACCAAGGGCTTGTATCAATGTTCTGTATCAATAAAGGCCCAAGGACATC 360
DB 307 CAGATCAAGGACCAAGGGCTTGTATCAATGTTCTGTATCAATCAACAAAGCCCAAGGACATG 366
OY 361 GTTCCCATGCAACAGATGATTTGACCTATCAGTGTGCTTAACCTTCACTCAACCTGAA 420
DB 367 ATTCCATCCACAGATGATTTGCACTGTCAGTGTGCTTAACCTTCACTCAACCTGAA 426
OY 421 ATAATGTAATCTTCTAATAGAAGCAAAATTTGGCATCAATAATTTGACCTGCTCATCC 480
DB 427 ATAATGTAATCTTCTAATAGAAGCAAAATTTGGCATCAATAATTTGACCTGCTCATCT 483
OY 481 ATACAAGGTTTCCCAAGACCAAGAGATGATTTTGGTAAAAACCGAATAATTCAGT 540
DB 484 ATACAGGTTTCCCAAGACCTTAAGAGATGAGTGTGTTTGGCTAAGAACCAAAATTTCACT 543
OY 541 ACTAATGTAATCTGTCATGCAAGCAAAATCTCAAAATATGTCACAGAACTTAACAGT 600
DB 544 ATGAGTATGTAATGTAATGCAAGAAATCTCAAGATATGTCACAGAACTTAACAGT 603
OY 601 TCTATCAGCTTGTCTCTCAGTCCGAGAG--CAAGCAATGTGAGCATCTTGTGTC 657
DB 604 TCCATCAGCTTGTCTCTCAGTCCGAGAGTGTGAGAGCAATGATGACCATCTTGTGATTT 663
OY 658 CTGCAACTGTGAGTCAATGAGCTTCCCTACCTTATATATAGATGCAATACGAA 717
DB 664 CTGGAACCTGACAGAGCGGCTTTTATCTTCACTTCTCTATAGA--GCTTGAGGAC 720

OY 718 CCCACCCCTGATGAGACACATCTCTGATTCGCGCTCTGCTTGTATGTTGTATTT 777
DB 721 CCGCAGCCTCCGCCAGACACCATCTCTGATTTACAGCTGTACTTCCAA--CAAGTATT 777
OY 778 TTGTGTGGATGAGTGTGTTCTTCTTAACACTAAGGAA--AGGAAAGAGACAGCCTGGC 834
DB 778 ATATGTGTGATGCTTTCTGCTTAATTTCTATGGAATGAGAGAAAGAGGCGCTCCG 837
OY 835 CCCTTCATGAATGTAAGCAACAAAGTGGAGAGAGAAAGAAAGTGAAGCCAAAGGA 894
DB 838 AACTCTTAATATGTGGAACACACAAATGAGAGGGAAGAGTGAACACAGACAGAA 897
OY 895 AGAGTCCGATACCATGAACGGAAGATCTGATGAAGCCAGTGTG--TTAACAATTTG 951
DB 898 AGAGAAATAATTCATATACCTGGAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTG 957
OY 952 AAGACAGCTTCAGGCGACAAACAGTACTAACAAGTTT 987
DB 958 AAGACATCTTCATGCGACAAAGTGAATGATGATTTT 993

RESULT 10
LOCUS ARI60450 1002 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 33 from patent US 6255073.
ACCESSION ARI60450
VERSION ARI60450.1 GI:16224366
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6255073-A 33 03-JUL-2001;
FEATURES
Source location/Qualifiers
1..1002
BASE COUNT 309 a 215 c 203 g 275 t
ORIGIN

Query Match 58.3%; Score 575.2; DB 6; Length 1002;
Best Local Similarity 77.8%; Pred. No. 6.7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

OY 1 ATGATCTCAGATGCACTATGAACTGAATAACATTTCTTTGTGATGACCCCTGCTC 60
DB 7 ATGATCCCCAGTGCACTATGGAAGTGAACAATTCCTTTGTGATGACCTTCTGCTC 66
OY 61 TATGTCGCTGCTTCCATGAAGTCAAGCATTTTCAAGACAGCTGAGAACTGCGATGC 120
DB 67 TCTGTCGCTGCTCTCTCTGAAGATTCAGCTTATTTCAATGAGAGCTCAACCTGCGATGC 126
OY 121 CATTTTAAATAATTCCAAAACATTAAGCCTGGATGAGTGGTGTGTTTGGCAGACCAAG 180
DB 127 CAATTTGCAAACTCTCAAAACCAAGCCTGAGTGAAGTGTATTTTGGCAGGACCAAG 186
OY 181 GATAAGCTGTTCTGTATGAGCTATACAGAGCAAGAGCAACCCCTCAAAATGTTATGCC 240
DB 187 GAAACCTGTTCTGATGAGTGAAGTACTTAAGGCAAGAAATTTGACAGTGTCTATTTCC 246
OY 241 AAGTATAGGGCCGACAGCTTTGACAAAGCAATTTGAGACCTTGAGACTTCATATATT 300
DB 247 AAGTATATGAGCCGACCAAGTTTTGTATTTGGACAGTGTGAGACCTTGACATCTT 306
OY 301 CAGATCAAGGACCAAGGGCTTGTATCAATGTTTCTTCATCATTAAGGCCCCAAGGACTC 360
DB 307 CAGATCAAGGACCAAGGGCTTGTATCAATGATTCATCATCAACAAAGGCCCAAGGAATG 366
OY 361 GTTCCCATGCAACAGATGATTTGACACTATCAGTGTGCTTAACCTTCACTCAACCTGAA 420
DB 367 ATTGCATCCACAGATGATTTGATGAGTGTGAGTGTGCTTGTCACTTCACTCACTGAA 426

QY	259	AGCTTTGACAAAGACATTTGGACCTGGAGCTCCCAATTAATTCACATCAAGGACAAAGGCG	318		
Db	241	AGCTTTGACCAAGCCACCTGGACCTGGAGACTCCCAACAGTTTCAATACAGGACCAAGGCG	300		
QY	319	TTGATCAATGTTTCGTTTCATCATCATTAAGAGGCGCCAAAGGACTGTTCCCATGACCCAGATG	378		
Db	301	TCATATCAATGTTTCATCATCATTAAGAGGCGCCAGATGACCTGTTCCATATCCACAGATG	360		
QY	379	AATTCGACCTATCAGTGTCTGCTAATTCAGTCAACTGAAATTAATGTAATCTTCAAT	438		
Db	361	AGTTCTGACCAATCATCTCTGCTAATTCAGTCAACTGAAATTAATCACTACTTCAAT	420		
QY	439	AGAACGAAATTTTCGGGACTCAATTAATTTGACCTGCTCATCCATCAAGGTTACCCAGAA	498		
Db	421	CACACGAAATTTCTG---TCATTAATTTGACCTGCTCATCTTCAACAAAGGCTACCCAGAA	477		
QY	499	CCCAAGAGATGATATTTTGGTAAACCCGAAATTCAGTCAAGTCAAGTATGATGCTGTC	558		
Db	478	CCCGAGAGATGATATGTTGGTAAATTCGAAAGATTCACACCTGAGAGATGATGCTGAC	537		
QY	559	ATGAAGAAATCTCAAAATTAATGTCACAGAACTCTCAACAGTTTCTATCAGCTTGCCTTC	618		
Db	538	ATGAAGAAATCTCAAAATTAATGTCACAGAACTCTCAACAGTTTCTATCAGCTTGCCTTC	597		
QY	619	TCAGACCTGAAAGCAAGATGTCAGCATTTTCGTGTCCTGCACTTGAGTCATGAA--	677		
Db	598	CCCATCTCTCCCGAGACAAATGTGAGCATGCTGTGTCTGTCGAACCTGAGCCAAAGCAAG	657		
QY	678	-----GCTTCCCTCCCTACCTTATTAATTAATGATGA---CATACGAAACCCACCCCTGAT	729		
Db	658	ACACGTCTTTCTCCCTACCTTATTAATTAATGATGCAAAAGCCACCTGTGCAACCCCTGTC	717		
QY	730	GGAGACCACTCTCTGGAATTCGGGCTCTGCTTGTAAATGTTGGTCATATTTTGTGSGATG	789		
Db	718	CCAGACCACTCTCTGGAATTCGACCTCTACTTGTAAACAGTGGTGTGTGTGTGGATG	777		
QY	790	GTGCTTCTTAACTCTAAGGAAAGAAAGAAAGACGCTGGCCCTCATGTAAT--	847		
Db	778	GTGCTTCTTGTAACTCTAAGGAAAGAAAGAAAGACGCTGGCCCTCATATTAATGT	837		
QY	848	-GTGAACCAACAAAGTGGAGAAAGAAAGAAAGTGAAGACCAAGAAAGATACGGTAC	906		
Db	838	GGTGAACCACTCAAAATTAATGAACGAAAGCGATGTAACAATTAACAGACAGAAAGTC	897		
QY	907	CATGAACGGAAGATCTGATGAGCCCAAGT---TGTAACTTTGAGACAGACTTCA	963		
Db	898	CAT-----GAACGATCTGATGATGCCCAAGTGTATTAATTTTAAAGCACACCTCA	951		
QY	964	GGCGACACAGTACTACACAGATT	987		
Db	952	GATGACACAGTACTACAGATT	975		
RESULT 8	ARI47736	1002 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	ARI47736				
DEFINITION	Sequence 33 from patent US 6225042.				
ACCESSION	ARI47736				
VERSION	ARI47736.1	GI:15111826			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1002)				
AUTHORS	Cal, Z., Spirent, J., Brunmark, A., Jackson, M. and Peterson, P.A.				
TITLE	Antigen presenting system and methods for activation of T-cells				
JOURNAL	Patent: US 6225042-A 33 01-MAY-2001;				
FEATURES	location/Qualifiers				
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BASE COUNT	309 a	215 c	203 g	275 t	
ORIGIN					

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1..978
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DELVFMODNLYVELYRQEKPRHVNYSKWGTSIDQKWTWLRHNVQIKRGST
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ORMVWLNTKSTEHADMRKSONNITELYNVIRSLPIPETNVSIVCLOLEPS
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BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 62.8%; Score 620; DB 4; Length 994;
Best Local Similarity 81.3%; Pred. No. 6e-156;
Matches 800; Conservative 0; Mismatches 160; Indels 24; Gaps 6;
QY 19 ATGAGCAATGAATTAACATCTCTCTTGATGAGACCCCTCCTCTATGTCCTCCATG 78
Db 1 ATGGAGCTGAGTACATCTCTTGATGAGTCCTCTCTGTCCTCTCTG 60
QY 79 AAGAGTCAAGCATATTTCAACAAGACTGAGAACGTCATTCATTTCAATTTCTCA 138
Db 61 AAAAGTCAGGCAATTTTCATATGAGACGAGAACGTCCTGCAATTTCAACGCGAG 120
QY 139 AACATAGCCTGGAGAGTGTGTGTTTGGCAGAGACAGAGATAGCTGCTGTAC 198
Db 121 AACCTAAGCCTGGATGAGCTGTCATATTTGGCAGAGACAGATTAACCTGCTCTAC 180
QY 199 GAGCTATACAGGCGAAAGAACCCCTCAAAATGTCATGCAAGATTAAGGCGCGACA 258
Db 181 GAGCTATACGAGGCGCAAGAGAACCCCTCAATGTTAATTCAGATATAGGCGCGACA 240
QY 259 AGCTTGAACAAGACAATTTGACCCCTGAGACTCATATATTCAGATCAAGACAAGGC 318
Db 241 AGCTTGAACAAGGCGACCGAGACCTGAGACTCCACAAAGCTCAATCAGAGACGCG 300
QY 319 TTGTATCAATGTTTGGTTCATATAAGGCGCAAGAGACTGCTCCATGCAAGATG 378
Db 301 TCATATCAATGTTTCAATTCATATAAGGCGGAGCTGCTGTTCTCTATCCACAGATG 360
QY 379 AATTCAGACTATCAGTGTGTCATCTCAGTCAACGTAATATATGTAATCTAT 438
Db 361 AGTTCAGACTATCAGTGTGTCATCTCAGTCAACGTAATATATCTACTAT 420
QY 439 AGAACAAGAAATTCGATCATATAATTTGACCTGCTCATCCATCAAGAGTACCAGAA 498
Db 421 CACACAGAAATTCG--TCATAAATTTGACCTGCTCATCTACACAAAGCTACCAAGA 477
QY 499 CCCAAGAGATGTTATTTTGGTAAAAACCGAGATTCAGTACTAGTATGATGTC 558
Db 478 CCCCAAGAGTGTATATGTTGCTAAATACGAGAAATTCACACCACTGAGCATGATGTCAG 537
QY 559 ATGAAGAAATTCGAAATATATGTCACAGAACTTACAGTTTCTATGCTGCTGCT 618
Db 538 ATGAAGAAATTCGAAATATATGTCACAGAACTTACAGTATCTATCAATCAGGCTGCTCTT 597

QY 619 TCAGTCCCTGAGCAAGCAATGTGAGCATCTCTGTCCTGCAACTGATCATGAA- 677
Db 598 CCATCCCTCCCGAGACAATGTGAGCATCTCTGTCCTGCAACTGAGCCACAGCAAG 657
QY 678 -----GCTTCCCTCCCTACCTTATATATAGATGA--CATACGAAGAACCCCTGAT 729
Db 658 AACATGCTTTTCTCCCTACCTTATATATAGATGAAGCAAGCAAGCAAGCCCTGTC 717
QY 730 GGAGACCAATCTCTCTGATTTGGGCTCTGCTGTATATGTTGTCATTTTGTGGATG 789
Db 718 CCAAGACCAATCTCTGATTTGGGCTCTGCTGTATATGTTGTCATTTTGTGGATG 777
QY 790 GTGTTCTTTCAACATAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 778 GTGTTCTTTTGAACATAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
QY 848 -GTGAACCAACAAAGTGAG 906
Db 838 GGTGAACCAACAAAGTGAG 897
QY 907 CATGAACGGAAGATCTGATGAAGCCAGT---TCTTAACATTTGAGAGAGAGAGAGAG 963
Db 908 CAT-----GAGCATCTGATGATGAGCCAGTGTATATATTTAAAGACAGCCTCA 951
QY 964 GCGCAACAGTACTACAGATTT 987
Db 952 GATGACCAAGTACTACAGATTT 975
RESULT 7
AX027016 994 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 13 from Patent WO0037102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE
ORGANISM
pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 994)
Rogers,N.J., Dorrington,A. and Lechler,R.I.
TITLE
Immunosuppression
JOURNAL
Patent: WO 0037102-A 13 JUN-2000;
ROGERS NICHOLA JANE (GB) ; DORRINGTON ANTHONY (GB) ; LECHLER ROBERT IAN (GB)
FEATURES
Location/Qualifiers
Source
1..994
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 62.8%; Score 620; DB 6; Length 994;
Best Local Similarity 81.3%; Pred. No. 6e-156;
Matches 800; Conservative 0; Mismatches 160; Indels 24; Gaps 6;
QY 19 ATGAGCAATGAATTAACATCTCTCTTGATGAGACCCCTCCTCTATGTCCTCCATG 78
Db 1 ATGGAGCTGAGTACATCTCTTGATGAGTCCTCTCTGTCCTCTCTG 60
QY 79 AAGAGTCAAGCATATTTCAACAAGACTGAGAACGTCATTCATTTCAATTTCTCA 138
Db 61 AAAAGTCAGGCAATTTTCATATGAGACGAGAACGTCCTGCAATTTCAACGCGAG 120
QY 139 AACATAGCCTGGAGAGTGTGTGTTTGGCAGAGACAGATAGCTGCTGTAC 198
Db 121 AACCTAAGCCTGGATGAGCTGTCATATTTGGCAGAGACAGGATTAACCTGCTCTAC 180
QY 199 GAGCTATACAGGCGAAAGAACCCCTCAAAATGTCATGCAAGATTAAGGCGCGACA 258
Db 181 GAGCTATACGAGGCGCAAGAGAACCCCTCATATATGTTAATTCAAAGTATATAGGCGACA 240

QY	728	ATGGAGACCAATCTCTGGATTTGGGCTCGCTCTGTAATGTTGGTCATTTGTGTGGGA	787
Db	799	AACAAGGCCACTCTCCCTGGATTGGGCTGTACTGTATGTTTGTGTTTTGTGGGA	858
QY	788	TGCTGTTCTTTTACACTAAGAAAGAGAAAGAACAGCAGCTTGCCCTCATGTAAAT	847
Db	859	TGCTGTTCTTTTAAACACTAAGAAAGAGAAAGAACAGCAGCTTGCCCTCATGTAAAT	918
QY	848	GTGAACCAACAACTGGAGAGAAAAGAAAGTGCACAGACCAAGAAAGAGTACGTAAC	907
Db	919	GTGAACCAACATCAAAAGGGAGAGAAAAGAGAGCAACAGCAACGAAGAGATCAATACC	978
QY	908	ATGAACGGAAGATCTGTATGAAGCCAGTGTTTACATTTTGAAGACAGCTTACGCG	967
Db	979	ACGTACTCGAGAGATCTGTATGAAGCCAGTGTTTACATTTTGAAGACAGCTTACGCG	1038
QY	968	ACAACAGT 975	
Db	1039	ACAAAAT 1046	
RESULT 5	AF106827	1795 bp	MAM 14-DEC-1999
LOCUS	AF106827		
DEFINITION	Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.		
ACCESSION	AF106827		
VERSION	AF106827.1	GI:5572518	
KEYWORDS	dog.		
SOURCE	Canis familiaris		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
REFERENCE	1 (bases 1 to 1795)		
AUTHORS	Yang, S. and Sim, G. K.		
TITLE	New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules		
JOURNAL	Immunogenetics 50 (5-6), 349-353 (1999)		
MEDLINE	20093996		
REFERENCE	2 (bases 1 to 1795)		
AUTHORS	Yang, S. and Sim, G. K.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA		
FEATURES	Location/Qualifiers		
Source	1..1795		
gene	/organism="Canis familiaris"		
5' UTR	/db_xref="taxon:9615"		
gene	/cell_type="peripheral blood mononuclear cells"		
1' UTR	1..1795		
gene	/gene="CD86"		
1' UTR	1..6		
gene	/gene="CD86"		
1' UTR	7..849		
gene	/gene="CD86"		
1' UTR	/function="counter-receptor for CD28 and CD152 (CTLA4)"		
gene	/note="lacks transmembrane domain; alternatively spliced"		
1' UTR	/codon_start=1		
gene	/product="truncated B7-2 protein"		
1' UTR	/protein_id="AAFI7298.1"		
gene	/db_xref="GI:6572519"		
1' UTR	/translation="MYRCIMELNLIFFVTLILYGAASKSQAFNFKTELPCHFTN		
gene	SQNSIDELVFWDDOKLVLLEYLRKKNPQVHRYKGRTSFDKDNWLRHNIQI		
1' UTR	KDGLVQCFVHHKGPGLVPMQHSNLSLVANFSQPEIWTNKRKENSQIINLTCS		
gene	IOGPERKEMVFLAKTENSSTKYDVTWKQSNVTELYNYSISLSEFVPSANVSI		
1' UTR	VLDESKRLPSLPYNIETNKRERESQGTREVRVYHETERSDEACVNIKSTASGNS		
gene	TTPQ"		
1' UTR	850..1795		
gene	/gene="CD86"		
BASE COUNT	592 a 366 c 347 g 490 t		
ORIGIN			
Query Match	71.3%	Score 704:	DB 4: Length 1795:
Best Local Similarity	99.3%	Pred. No. 1.5e-178:	

	Matches	70%	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
OY	1	ATGTAATCAGATGCACATCATGAACCTAATAACAATTCTTTGTGGATGCCCTCGTCC	60							
Dd	7	ATGTAATCAGATGCACATCATGAACCTAATAACAATTCTTTGTGGATGCCCTCGTCC	66							
OY	61	TATGTCGCTTCCTCATTAAGAATCAAGCATATTTCAAACAAGACTGGAACTGCCATGC	120							
Dd	67	TATGTCGCTTCCTCATTAAGAATCAAGCATATTTCAAACAAGACTGGAACTGCCATGC	126							
OY	121	CATTTCACAAATTCCCAACAATATAAGCTGGATAGTGAGTAGTTTTGGCAGACCAC	180							
Dd	127	CATTTCACAAATTCCCAACAATATAAGCTGGATAGTGAGTAGTTTTGGCAGACCAC	186							
OY	181	GATAAGCTGGTTCTGTACAGCTATACAGAGSCAAAGAACCCCTCAAAATGTTCATGCG	240							
Dd	187	GATAAGCTGGTTCTGTACAGCTATACAGAGSCAAAGAACCCCTCAAAATGTTCATGCG	246							
OY	241	AAGTTAAAGGGCCGCACACAGCTTTGACAAAGCAATTBGACCTTGAGACTCCATAATATT	300							
Dd	247	AAGTTAAAGGGCCGCACACAGCTTTGACAAAGCAATTBGACCTTGAGACTCCATAATATT	306							
OY	301	CAGATCAAGGACCAAGGGGCTTGATCAATGTTTCGTTCAATPAAAAGGGCCCCAAGGACATC	360							
Dd	307	CAGATCAAGGACCAAGGGGCTTGATCAATGTTTCGTTCAATPAAAAGGGCCCCAAGGACATC	366							
OY	361	GTTCCCATGCAACAGATGAATTTGCACCTATACAGTCAGTGTCTTAACCTCAGTCAACCTGAA	420							
Dd	367	GTTCCCATGCAACAGATGAATTTGCACCTATACAGTCAGTGTCTTAACCTCAGTCAACCTGAA	426							
OY	421	ATATATGTAACCTTTCAATAGAACAGAAAAATTCGTGGCATCATAAATTTGACCTGCTCATCC	480							
Dd	427	ATAAAGTAACCTTTCAATAGAACAGAAAAATTCGTGGCATCATAAATTTGACCTGCTCATCC	486							
OY	481	ATACAGGTTCCCAAGAACCCACAGAGATGTATTTTTGGTAAAACCGAGAAATTCAGT	540							
Dd	487	ATACAGGTTCCCAAGAACCCACAGAGATGTATTTTTGGTAAAACCGAGAAATTCAGT	546							
OY	541	ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATATATGACACAGAACTCTACAACTT	600							
Dd	547	ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATATATGACACAGAACTCTACAACTT	606							
OY	601	TCTATCACCTTGCTCTTCTCAGTCCCTGBAAGCAATGTGAGCATCTTCTGTGCTCG	660							
Dd	607	TCTATCACCTTGCTCTTCTCAGTCCCTGBAAGCAATGTGAGCATCTTCTGTGCTCG	666							
OY	661	CAACTGTGTCGAATGAAGCTTCGCCCTACTATATATATAGATGACACATA	712							
Dd	667	CAACTGTGTCGAATGAAGCTTCGCCCTACTATATATATAGATGACACACATA	718							
RESULT 6 PIGD86g										
LOCUS	PIGD86g	Sus scrofa CD86 mRNA, complete cds.	994 bp	mRNA	linear	MAM 17-JUN-1997				
DEFINITION	L/76099									
VERSION	L76099.1	GI:2198558								
KEYWORDS	pig.	T cell costimulation.								
SOURCE										
ORGANISM	Sus scrofa	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;								
REFERENCE	Authors	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 994)								
TITLE	JOURNAL MEDLINE COMMENT FEATURES	Porcine endothelial CD86 is a major costimulator of xenogeneic human T cells: cloning, sequencing, and functional expression in J. Immunol. 157 (9), 3838-3844 (1996) GSDB:S:74002								
		Location/Qualifiers								
		I..994								

QY	314	AGGCGCTGTATCAATGTTTGGTTCATCATTAAGAGGCCCCAAGAGACTGGTCCCATATGCACC	373
Db	495	AGGGCACTATACACTGTTTTCATCATTAATAAGAGGCCCCAAGAGACTATGTTCCCATATGCACC	554
QY	374	AGATGAATTCAGACCTATCACTGCTTGGCTAACTTCAGTCAACCTGAAATTAATGATGACTT	433
Db	555	AAATGAGTTGTGACCTATCACTGCTTGGCTAACTTCAGTCAACCTGAAATTAATGATGACTT	614
QY	434	CTAATAGAACAGAAATTTCTGGCATCATTAATTTGACTGCTCATCCATACAAGTTACC	493
Db	615	CTAATAGAACAGAAATTTCTGGCATCATTAATTTGACTGCTCATCCATACAAGTTACC	674
QY	494	CAGAACCCAAAGAGATGATTTTGGTAAACCGAGATTAAGTCAAGTCAAGTATGATA	553
Db	675	CAGAACCCAAAGAGATGATTTTGGTAAACCGAGATTAAGTCAAGTCAAGTATGATA	734
QY	554	CTGTATGAGAAATTCATAAATTAATGTACAGAACTCTACAGCTTTCTATCAGCTTGT	613
Db	735	CTGTATGAGAAATTCATAAATTAATGTACAGAACTCTACAGCTTTCTATCAGCTTGT	794
QY	614	CCCTTCAGTCCCTGAAGACCAAGCAATGTGACATCTCTGTGCTCCCTGACACTGAGTCAA	673
Db	795	CTTTTTCAGTCCCTGAAGACCAAGCAATGTGACATCTCTGTGCTCCCTGACACTGAGTCAA	854
QY	674	T---GAAGCTTCCCTCCCTACCTTATAATATAGATGACACA---TACGAACCCACCCCTG	727
Db	855	TGAGATATCTCTCTCCCTACCTTATAATATAGATGACACACCTCAAGATTAAGACCCCTG	914
QY	728	ATGGAAGCCACATCTCTCGAATTTGGGCTCTGCTTGTATGTGTCAATTTTGTGTGGGA	787
Db	915	AACAAGGCACTCTCTCGAATTTGGGCTCTGCTTGTATGTGTCAATTTTGTGTGGGA	974
QY	788	TGCTGTTCTTTCTTAACATAAGAGAAAGAGAAAGAACACACCTGGCCCTCTCATGTAT	847
Db	975	TGCTGTTCTTTCTTAACATAAGAGAAAGAGAAAGAACACACCTGGCCCTCTCATGTAT	1034
QY	848	GTGAACCAACAAAGTGGAGAGAAAAGAAAGTGGACAGACCAAGAGAAAGATGCGGTACC	907
Db	1035	GTGAACCAACATCAAAAGGAGAGAAAAGAGAACCAACACCAAGAGATGCGGTACC	1094
QY	908	ATGAAGACGAAGAATCTGATGAAGCCCGAGTGGTAAATTTGGAAGACAGCTTCAGGCG	967
Db	1095	ACGTACCTCGAAGATCTGATGAAGCCCGAGTGGTAAATTTGGAAGACAGCTTCAGGCG	1154
QY	968	ACAACAGTACTACACAGTTT 987	
Db	1155	ACAACAGTACTACACATTTT 1174	
RESULT 4			
LOCUS	AF157827	1138 bp	linear
DEFINITION	Felis catus CD86 antigen (CD86) mRNA, complete cds.		MAM 08-MAY-2000
ACCESSION	AF157827		
VERSION	AF157827.1	GI:5381423	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
1	Felis catus		
2	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
3	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
4	Choi,I.-S., Hash,S.M., Winslow,B.J. and Collisson,E.W.		
5	Sequence analyses of feline B7 costimulatory molecules		
6	Ver. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)		
7	Medline		
8	10713336		
9	2 (bases 1 to 1138)		
10	Choi,I.-S., Hash,S.M., Winslow,B.J. and Collisson,E.W.		
11	Direct Submission		
12	Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M		
13	University, Bldg. 1197 Km. 222, College Station, TX 77843, USA		
14	Location/Qualifiers		

source	1. .1138	/organism="Felis catus"
gene	/db.xref="taxon:9685"	
CDS	1. .1138	
	/gene="CD86"	
	63. .1052	
	/gene="CD86"	
	/note="B7-2 antigen"	
	/codon_start=1	
	/product="CD86 antigen"	
	/protein_id="AAd4294.1"	
	/db.xref="GI:5381424"	
	/translation="MGICDSTMGLSHTLLVMALLISGVSSMKSOAYFNKGTDELPCNPT NSQSIADLVEWODODKLVLYEIFRGENPQVHLKYGRTSFEDKNTLRILHNO IKRGPHCFHFKRPGKGLVPMHOMSDSLVIANFSDPELTIVSNPENGSIILTCS SIOCPKPKMYRQIANTENSTYKYDTPYMKRSQNNVLELVSTISLSPSEAHNVSE CALLETLEMLISLPENIDAPKDKDEQGHFLMIAVLVLFVYFCGMVFKTLRRKK KQDPSEHEETILKREKESKQINERYVPHVPERSEDAQCNILKTASGDKNO"	
BASE COUNT	358 a 245 c 246 g 289 t	
ORIGIN		
Query Match	78.5%; Score 774.4; DB 4; Length 1138;	
Query Similarity	88.9%; Pred. No. 1.8e-197;	
Matches 861; Conservative	0; Mismatches 101; Indels 6; Gaps 2;	
14	GCACATGGAACGTGAATACATTCCTTTGATGATGACCCCTCGCTCTATGATGCTGCTT	73
Db	GCACATATGGAGCTAGTCACACTCTCTTTGATGATGACCCCTCGCTCTATGATGCTGCTT	138
79	GCACATATGGAGCTAGTCACACTCTCTTTGATGATGACCCCTCGCTCTATGATGCTGCTT	138
74	CCATGCAAGATGACATATTTCAACAAGACTGGGAACCTGCCATGTCATTTACAATT	133
139	CCATGCAAGATGACATATTTCAACAAGACTGGGAACCTGCCATGTCATTTACAACT	198
134	CTCAAAACATTAAGCTGTGATGATGTTGTAGTCTTTGGCAGAGCCAGGATTAAGCTGTTT	193
Db	CTCAAAACATTAAGCTGTGATGATGTTGTAGTCTTTGGCAGAGCCAGGATTAAGCTGTTT	258
194	TGTACGACCTATACGAGGCAAGAAACCTCAAAATGTTTCATGCGCAAGTAAAGGCC	253
Db	TGTATGAGATATTTTCAGAGCAAAAGAAACCCCTCAAAATGTTTCATGCGCAAAATTAAGGCC	318
259	TGTATGAGATATTTTCAGAGCAAAAGAAACCCCTCAAAATGTTTCATGCGCAAAATTAAGGCC	318
254	GCACAGCTTTGACAAACACAAATTTGAGCCCTGAGACTCCATTAATTTGATGATCAAGGACA	313
Db	GTCACAGCTTTGACAAAGCAACCTGACCTGAGACTCCACATGTTAGATCAAGGACA	378
319	GTCACAGCTTTGACAAAGCAACCTGACCTGAGACTCCACATGTTAGATCAAGGACA	378
314	AGGGCTTGTATCAATGTTTCGTTTCATCATTAAGGGGCCCAAGAGACTGTTCCCATGACCC	373
Db	AGGGCAATATCACTGTTTCATTCATTAATTAAGGGGCCCAAGAGACTGTTCCCATGACCC	438
374	AGATATATTTGACACTATACAGCTGCTGCTAATCTAGTCAACCTGAATTAATGTTACTT	433
Db	AAATAGTGTGACCTATACAGCTGCTGCTAATCTAGTCAACCTGAATTAATGTTACTT	498
434	CTAATGAGAACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCATACAAAGTTTACC	493
Db	CTAATGAGAACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCATACAAAGTTTACC	558
494	CAGAACCCAGAGAGATGTTATTTTTGGTAAAAACCGAATTTCAAGTACTAAGTATGATA	553
Db	CAGAACCCAGAGAGATGTTATTTTTGGTAAAAACCGAATTTCAAGTACTAAGTATGATA	618
554	CTGTATGAGAAATCTCAAAATATATGTCACGAACTGTACAACTTTCTATACACTTGT	613
Db	CTGTATGAGAAATCTCAAAATATATGTCACGAACTGTACAACTTTCTATACACTTGC	678
614	CTTCTCAGTCCCTCGAAGCAAGCAATGTGACATCTTCTGTGTCCTGCACACTTGAAGTCAA	673
Db	CTTCTCAGTCCCTCGAAGCAAGCAATGTGACATCTTCTGTGTCCTGCACACTTGAAGTCAA	738
674	T---GAAGTTCCTCCCTACCTTAAATATGATGACACA---TACGAACCCACCCCGG	727
Db	TGGAATGCTGCTCTCCCTACCTTCAATATATGATGACACAACCTTAAGATTAAGACCTTG	798

polyA_signal	1245.	.1250			
BASE COUNT	378 a	281 c	260 g	351 t	
ORIGIN					

Source	1. 1897	/organism="Canis familiaris"	/db_xref="taxon:9615"	/cell_type="peripheral blood mononuclear cells"
gene	1. 1897	/gene="CD86"		
5'UTR	1..5	/gene="CD86"		
CDS	6..995	/gene="CD86"		
		/function="counter-receptor for CD28 and CD152 (CTLA4)"		
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		/product="B7-2 protein"		
		/protein_id="AA17297.1"		
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	996..1897			
3'UTR		/gene="CD86"		
BASE COUNT	585 a 400 c 383 g 529 t			
ORIGIN				
Query Match	100.0%; Score 987; DB 4; Length 1897;			
Best Local Similarity	100.0%; Pred. No. 1,2e-254;			
Matches	987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGTATCTCAGATGACATGAGAACTGTAATAACATTTCTTTGGATGACCCCTGCTGC	60	
DB	6	ATGTATCTCAGATGACATGAGAACTGTAATAACATTTCTTTGGATGACCCCTGCTGC	65	
QY	61	TATGGTGGCTGCTTCATGAAGTCAAGTCAACATTTCCACAAGACTGAGAACTGGCATGC	120	
DB	66	TATGGTGGCTGCTTCATGAAGTCAAGTCAACATTTCCACAAGACTGAGAACTGGCATGC	125	
QY	121	CATTTTACAATTTCTCAAAACATTAAGCCTGGATGAGTGTGTTGGCAGAGCCAG	180	
DB	126	CATTTTACAATTTCTCAAAACATTAAGCCTGGATGAGTGTGTTGGCAGAGCCAG	185	
QY	181	GATAAGCTGGTTCGTGTACGAGCTATACAGAGGCAAGAAACCTCAAAATGTTCATGCG	240	
DB	186	GATAAGCTGGTTCGTGTACGAGCTATACAGAGGCAAGAAACCTCAAAATGTTCATGCG	245	
QY	241	AAGTATTAAGGGCCGACAGAGCTTTGCACAAACACATTTGGACCCCTGAGACTCATATATTT	300	
DB	246	AAGTATTAAGGGCCGACAGAGCTTTGCACAAACACATTTGGACCCCTGAGACTCATATATTT	305	
QY	301	CAGATCAAGGACCAAGGGCTTTATCAATGTTTCGTTCAATTAAGGGCCCAAGAGACTC	360	
DB	306	CAGATCAAGGACCAAGGGCTTTATCAATGTTTCGTTCAATTAAGGGCCCAAGAGACTC	365	
QY	361	GTTCGCATGACACAGATGAATTCGACCTATACAGTGTGTTGAACCTTCAGTCAACCTGAA	420	
DB	366	GTTCGCATGACACAGATGAATTCGACCTATACAGTGTGTTGAACCTTCAGTCAACCTGAA	425	
QY	421	ATAATGGTAACCTCTCAATATAGAAGCAAAATTCGTGCATCATTAATTTGACCTGCTCATCC	480	
DB	426	ATAATGGTAACCTCTCAATATAGAAGCAAAATTCGTGCATCATTAATTTGACCTGCTCATCC	485	
QY	481	ATPACAGGTATCCAGAACCCAGAGAGATGTATTTTTTGGTAAAAACCGAGAATTCAGAT	540	
DB	486	ATPACAGGTATCCAGAACCCAGAGAGATGTATTTTTTGGTAAAAACCGAGAATTCAGAT	545	
QY	541	ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTACAGAACTACAAAGTT	600	
DB	546	ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATTAATGTACAGAACTACAAAGTT	605	
QY	601	TCATACACCTGCTCTCTTCTCAGTCCCTTAAGCAAGCATGTGAGATCTTGTGTCTGTG	660	
DB	606	TCATACACCTGCTCTCTTCTCAGTCCCTTAAGCAAGCATGTGAGATCTTGTGTCTGTG	665	

QY	661	CAAATGGTCATGAAGACCTTCCCTCCCTACCTATATATAGATGCAATACGAAACC	720
Db	666	CAACTTGATGAATGAAGACCTTCCCTCCCTACCTATATATAGATGCAATACGAAACC	725
QY	721	ACCCCTGATGAGAGACCAATCCTCTGATGTCGGCTCTGCTGTATGTTGGTCATTYTG	780
Db	726	ACCCCTGATGAGAGACCAATCCTCTGATGTCGGCTCTGCTGTATGTTGGTCATTYTG	785
QY	781	TGTGGGATGCTGTTCTTCTTAACACTAAGGAAAGAAAGAACAGACCTGGCCCCCTCT	840
Db	786	TGTGGGATGCTGTTCTTCTTAACACTAAGGAAAGAAAGAACAGACCTGGCCCCCTCT	845
QY	841	CATGATGTTGAAACCAACAAAGTGGAGGAAAGAAAGAAATGAGCAGACCAAGAAAGATA	900
Db	846	CATGATGTTGAAACCAACAAAGTGGAGGAAAGAAAGAAATGAGCAGACCAAGAAAGATA	905
QY	901	CGGTACCATGGAAGGAAAGATCTGATATAGCCAGTGTGTATACATTTCGAAGACAGCT	960
Db	906	CGGTACCATGGAAGGAAAGATCTGATATAGCCAGTGTGTATACATTTCGAAGACAGCT	965
QY	961	TCAGGCGACAACAGTACTACACAGTTT 987	
Db	966	TCAGGCGACAACAGTACTACACAGTTT 992	
RESULT 2			
AB030652			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
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AUTHORS			
TITLE			
JOURNAL			
COMMENT			
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Title: US-09-646-561-9

Perfect score: 987
Sequence: 1 atgctctcagatgcactat.....acaacagctactacacagttt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_cm:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	ID	Description
8				

1	987	100.0	1897	4	AF106826	AF106826 Canis fam
2	786.4	79.7	1270	4	AB030652	AB030652 Felis cat
3	784.8	79.5	2830	4	AY007704	AY007704 Felis cat
4	774.4	78.5	1138	4	AF157827	AF157827 Felis cat
5	704	71.3	1795	4	AF106827	AF106827 Canis fam
6	620	62.8	994	4	P16CD865	L76099 Sus scrofa
7	620	62.8	994	6	AX027016	AX027016 Sequence
8	575.2	58.3	1002	6	AR147736	AR147736 Sequence
9	575.2	58.3	1002	6	AR159758	AR159758 Sequence
10	575.2	58.3	1002	6	AR160450	AR160450 Sequence
11	575.2	58.3	1112	6	HUM872A	L25259 Human CTLA4
12	575.2	58.3	1120	6	AR030780	AR030780 Sequence
13	575.2	58.3	1120	6	AR112747	AR112747 Sequence
14	575.2	58.3	1120	6	AR146413	AR146413 Sequence
15	575.2	58.3	1120	6	AX047043	AX047043 Sequence
16	575.2	58.3	1161	6	AR146414	AR146414 Sequence
17	570.2	57.8	1424	6	AX330924	AX330924 Sequence
18	570.2	57.8	1424	6	AX332506	AX332506 Sequence
19	570.2	57.8	1424	6	HSU04343	U04343 Human CD86
20	570.2	57.8	2205	6	AX188198	AX188198 Sequence
21	565.2	57.3	972	6	AX027005	AX027005 Sequence
22	561.6	56.9	1048	9	AF344857	AF344857 Macaca mu
23	560.6	56.8	1062	9	AF344861	AF344861 Cercopit
24	554.2	56.1	1062	9	AF344840	AF344840 Cercopit
25	552.6	56.0	1042	9	AF344851	AF344851 Macaca ne
26	537.2	54.4	1156	4	RABCD86B	D49842 Rabbit mRNA
27	466.8	47.3	924	4	BT4291475	AJ291475 Bos tauru
28	463.8	47.0	751	6	AR147737	AR147737 Sequence
29	463.8	47.0	751	6	AR159759	AR159759 Sequence
30	463.8	47.0	751	6	AR160451	AR160451 Sequence
31	453.8	46.0	738	6	AX002781	AX002781 Sequence
32	453.8	46.0	738	6	AX149548	AX149548 Sequence
33	447.2	45.3	901	9	AF344836	AF344836 Papio cyn
34	344.4	34.9	930	6	AX027012	AX027012 Sequence
35	344.4	34.9	984	10	AF065897	AF065897 Mus muscu
36	344.4	34.9	984	10	AF065898	AF065898 Mus muscu
37	344.4	34.9	984	10	AF065899	AF065899 Mus muscu
38	344.4	34.9	984	10	AF065900	AF065900 Mus muscu
39	344.4	34.9	1115	10	S70108	S70108 early T cel
40	344.4	34.9	1151	6	AR030781	AR030781 Sequence
41	344.4	34.9	1151	6	AR146412	AR146412 Sequence
42	344.4	34.9	1163	6	AR112764	AR112764 Sequence
43	344.4	34.9	1183	10	M05B72X	L25606 Murine B7-2
44	339.6	34.4	2528	10	BC013807	BC013807 Mus muscu
45	337.2	34.2	1261	6	AR146408	AR146408 Sequence

ALIGNMENTS

RESULT 1
AF106826 LOCUS 1897 bp mRNA, linear MAY 14-DEC-1999
DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106826
VERSION AF106826.1 GI:6572516
KEYWORDS
SOURCE
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1897)
AUTHORS Yang, S. and Sim, G.-K.
TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093996
REFERENCE 2 (bases 1 to 1897)
AUTHORS Yang, S. and Sim, G.-K.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers